Mouse Dnmt3a DNA sequence

1 GAATTCCGGC CTGCTGCCGG GCCGCCCGAC CCGCCGGGCC ACACGGCAGA
51 GCCGCCTGAA GCCCAGCGCT GAGGCTGCAC TTTTCCGAGG GCTTGACATC
101 AGGGTCTATG TTTAAGTCTT AGCTCTTGCT TACAAAGACC ACGGCAATTC
151 CTTCTCTGAA GCCCTCGCAG CCCCACAGCG CCCTCGCAGC CCCAGCCTGC
201 CGCCTACTGC CCAGCAATGC CCTCCAGCGG CCCCGGGGAC ACCAGCAGCT
251 CCTCTCTGGA GCGGGAGGAT GATCGAAAGG AAGGAGAGGA ACAGGAGGAG
301 AACCGTGGCA AGGAAGAGCG CCAGGAGCCC AGCGCCACGG CCCGGAAGGT
351 GGGGAGGCCT GGCCGGAAGC GCAAGCACCC ACCGGTGGAA AGCAGTGACA
401 CCCCCAAGGA CCCAGCAGTG ACCACCAAGT CTCAGCCCAT GGCCCAGGAC
451 TCTGGCCCCT CAGATCTGCT ACCCAATGGA GACTTGGAGA AGCGGAGTGA
501 ACCCCAACCT GAGGAAGGGA GCCCAGCTGC AGGGCAGAAG GGTGGGGCCC
551 CAGCTGAAGG AGAGGGAACT GAGACCCCAC CAGAAGCCTC CAGAGCTGTG
601 GAGAATGGCT GCTGTGTGAC CAAGGAAGGC CGTGGAGCCT CTGCAGGAGA
651 GGGCAAAGAA CAGAAGCAGA CCAACATCGA ATCCATGAAA ATGGAGGGCT
701 CCCGGGGCCG ACTGCGAGGT GGCTTGGGCT GGGAGTCCAG CCTCCGTCAG
751 CGACCCATGC CAAGACTCAC CTTCCAGGCA GGGGACCCCT ACTACATCAG
801 CAAACGGAAA CGGGATGAGT GGCTGGCACG TTGGAAAAGG GATGCTGAGA
851 AGAAAGCCAA GGTAATTGCA GTAATGAATG CTGTGGAAGA GAACCAGGCC
901 TCTGGAGAGT CTCAGAAGGT GGAGGAGGCC AGCCCTCCTG CTGTGCAGCA
951 GCCCACCGAC CCTGCTTCTC CGACTGTGGC CACCACCCCT GAGCCAGTAG
1001 GAGGGGATGC TGGGGACAAG AATGCTACCA AAGCACCCGA CGATGAGCCT
1051 GAGTATGAGG ATGGCCGGGG CTTTGGCATT GGAGAGCTGG TGTGGGGGAA
1101 ACTTCGGGGT TTCTCTTGGT GGCCAGGCCG AATTGTGTCT TGGTGGATGA

FIG. 1A-1

AMENDED SHEET

1151 CAGGCCGGAG CCGAGCAGCT GAAGGCACTC GCTGGGTCAT GTGGTTCGGA

1201 GATGGCAAGT TCTCAGTGGT GTGTGTGGAG AAGCTCATGC CCCTGAGCTC

1251 CTTCTGCAGT GCATTCCACC AGGCCACCTA CAACAAGCAG CCCATGTACC

1301 GCAAAGCCAT CTACGAAGTC CTCCAGGTGG CCAGCAGCCG TGCCGGGAAG

1351 CTGTTTCCAG CTTGCCATGA CAGTGATGAA AGTGACAGTG GCAAGGCTGT

1401 GGAAGTGCAG AACAAGCAGA TGATTGAATG GGCCCTCGGT GGCTTCCAGC

1451 CCTCGGGTCC TAAGGGCCTG GAGCCACCAG AAGAAGAGAA GAATCCTTAC

1501 AAGGAAGTTT ACACCGACAT GTGGGTGGAG CCTGAAGCAG CTGCTTACGC

1551 CCCACCCCCA CCAGCCAAGA AACCCAGAAA GAGCACAACA GAGAAACCTA

1601 AGGTCAAGGA GATCATTGAT GAGCGCACAA GGGAGCGGCT GGTGTATGAG

1651 GTGCGCCAGA AGTGCAGAAA CATCGAGGAC ATTTGTATCT CATGTGGGAG

1701 CCTCAATGTC ACCCTGGAGC ACCCATTCTT CATTGGAGGC ATGTGCCAGA

1751 ACTGTAAGAA CTGCTTCTTG GAGTGTGCTT ACCAGTATGA CGACGATGGG

1801 TACCAGTCCT ATTGCACCAT CTGCTGTGGG GGGCGTGAAG TGCTCATGTG

1851 TGGGAACAAC AACTGCTGCA GGTGCTTTTG TGTCGAGTGT GTGGATCTCT

1901 TGGTGGGGCC AGGAGCTGCT CAGGCAGCCA TTAAGGAAGA CCCCTGGAAC

1951 TGCTACATGT GCGGGCATAA GGGCACCTAT GGGCTGCTGC GAAGACGGGA

2001 AGACTGGCCT TCTCGACTCC AGATGTTCTT TGCCAATAAC CATGACCAGG

2051 AATTTGACCC CCCAAAGGTT TACCCACCTG TGCCAGCTGA GAAGAGGAAG

2101 CCCATCCGCG TGCTGTCTCT CTTTGATGGG ATTGCTACAG GGCTCCTGGT

2151 GCTGAAGGAC CTGGGCATCC AAGTGGACCG CTACATTGCC TCCGAGGTGT

2201 GTGAGGACTC CATCACGGTG GGCATGGTGC GGCACCAGGG AAAGATCATG

2251 TACGTCGGGG ACGTCCGCAG CGTCACACAG AAGCATATCC AGGAGTGGGG

2301 CCCATTcGAC cTGGTGATTG GAGGCAGTCC CTGCAATGAC CTcTCCATTG

FIG. 1A-2

2351 TCAACCCTGC CCGCAAGGGA CTTTATGAGG GTACTGGCCG CCTCTTCTTT

2401 GAGTTCTACC GCCTCCTGcA TGATGCGCGG CCCAAGGAGG GAGATGATCC

2451 CCCCTTCTTC TGGCTCTTTG AGAATGTGGT GGCCATGGGC GTTAGTGACA

2501 AGAGGGACAT CTCGCGATTT CTTGAGTCTA ACCCCGTGAT GATTGACGCC

2551 AAAGAAGTGT CTGCTGCACA CAGGGCCCGT TACTTCTGGG GTAACCTTCC

2601 TGGCATGAAC AGGCCTTTGG CATCCACTGT GAATGATAAG CTGGAGCTGC

2651 AAGAGTGTCT GGAGCACGGC AGAATAGCCA AGTTCAGCAA AGTGAGGACC

2701 ATTACCACCA GGTCAAACTC TATAAAGCAG GGCAAAGACC AGCATTTCCC

2751 CGTCTTCATG AACGAGAAGG AGGACATCCT GTGGTGCACT GAAATGGAAA

2801 GGGTGTTTGG CTTCCCCGTC CACTACACAG ACGTCTCCAA CATGAGCCGC

2851 TTGGCGAGGC AGAGACTGCT GGGCCGATCG TGGAGCGTGC CGGTCATCCG

2901 CCACCTCTTC GCTCCGCTGA AGGAATATTT TGCTTGTGTG TAAGGGACAT

2951 GGGGGCAAAC TGAAGTAGTG ATGATAAAAA AGTTAAACAA ACAAACAAAC

3001 AAAAAAACAAA ACAAAACAAT AAAACACCAA GAACGAGAGG ACGGAGAAAA

3051 GTTCACCACC CAGAAGAGAA AAAGGAATTT AAAGCAAACC ACAGAGGAGG

3101 AAAACGCCGG AGGGCTTGGC CTTGCAAAAG GGTTGGACAT CATCTCCTGA

3151 GTTTTCAATG TTAACCTTCA GTCCTATCTA AAAAGCAAAA TAGGCCCCTC

3201 CCCTTCTTCC CCTCCGGTCC TAGGAGGCGA ACTTTTTGTT TTCTACTCTT

3251 TTTCAGAGGG GTTTTCTGTT TGTTTGGGTT TTTGTTTCTT GCTGTGACTG

3301 AAACAAGAGA GTTATTGCAG CAAAATCAGT AACAACAAAA AGTAGAAATG

3351 CCTTGGAGAG GAAAGGGAGA GAGGGAAAAT TCTATAAAAA CTTAAAATAT

3401 TGGTTTTTTT TTTTTTTCCT TTTCTATATA TCTCTTTGGT TGTCTCTAGC

3451 CTGATCAGAT AGGAGCACAA ACAGGAAGAG AATAGAGACC CTCGGAGGCA

3501 GAGTCTCCTC TCCCACCCCC CGAGCAGTCT CAACAGCACC ATTCCTGGTC FIG. 1A-3

AMENDED SHEET

3551 ATGCAAAACA GAACCCAACT AGCAGCAGGG CGCTGAGAGA ACACCACACC
3601 AGACACTTTC TACAGTATTT CAGGTGCCTA CCACACAGGA AACCTTGAAG
3651 AAAACCAGTT TCTAGAAGCC GCTGTTACCT CTTGTTTACA GTTTATATAT
3701 ATATGATAGA TATGAGATAT ATATATATAA AAGGTACTGT TAACTACTGT
3751 ACATCCCGAC TTCATAATGG TGCTTTCAAA ACAGCGAGAT GAGCAAAGAC
3801 ATCAGCTTCC GCCTGGCCCT CTGTGCAAAG GGTTTCAGCC CAGGATGGGG
3851 AGAGGGGAGC AGCTGGAGGG GGTTTTAACA AACTGAAGGA TGACCCATAT
3901 CACCCCCCAC CCCTGCCCCA TGCCTAGCTT CACCTGCCAA AAAGGGGCTC
3951 AGCTGAGGTG GTCGGACCCT GGGGAAGCTG AGTGTGGAAT TTATCCAGAC
4001 TCGCGTGCAA TAACCTTAGA ATATGAATCT AAAATGACTG CCTCAGAAAA
4051 ATGGCTTGAG AAAACATTGT CCCTGATTTT GAATTCGTCA GCCACGTTGA
4101 AGGCCCCTTG TGGGATCAGA AATATTCCAG AGTGAGGGAA AGTGACCCGC
4151 CATTAACCCC NCCTGGAGCA AATAAAAAAA CATACAAAAT GT

FIG. 1A-4

AMENDED SHEET

Mouse Dnmt3b1 DNA Sequence

```
   1 GAATTCCGGG CGCCGGGGTT AAGCGGCCCA AGTAAACGTA GCGCAGCGAT
  51 CGGCGCCGGA GATTCGCGAA CCCGACACTC CGCGCCGCCC GCCGGCCAGG
 101 ACCCGCGGCG CGATCGCGGC GCCGCGCTAC AGCCAGCCTC ACGACAGGCC
 151 CGCTGAGGCT TGTGCCAGAC CTTGGAAACC TCAGGTATAT ACCTTTCCAG
 201 ACGCGGGATC TCCCCTCCCC CATCCATAGT GCCTTGGGAC CAAATCCAGG
 251 GCCTTCTTTC AGGAAACAAT GAAGGGAGAC AGCAGACATC TGAATGAAGA
 301 AGAGGGTGCC AGCGGGTATG AGGAGTGCAT TATCGTTAAT GGGAACTTCA
 351 GTGACCAGTC CTCAGACACG AAGGATGCTC CCTCACCCCC AGTCTTGGAG
 401 GCAATCTGCA CAGAGCCAGT CTGCACACCA GAGACCAGAG GCCGCAGGTC
 451 AAGCTCCCGG CTGTCTAAGA gGGAGGTCTC CAgCCTTCTG AATTACACGC
 501 AGGACATGAC AGGAGATGGA GACAGAGATG ATGAAGTAGA TGATGGGAAT
 551 GGCTCTGATA TTCTAATGCC AAAGCTCACC CGTGAGACCA AGGACACCAG
 601 GACGCGCTCT GAAAGCCCGG CTGTCCGAAC CCGACATAgC AATGGGACCT
 651 CCAGCTTGGA CAGGCAAAGA GCCTCCCCCA gAATCACCCG AGGTCGGCAG
 701 GGCCGCCACC ATGTGCAGGA GTACCCTGTG GAGTTTCCGG CTACCAGGTC
 751 TCGGAGACGT CGAGCATCGT CTTCAGCAAG CACGCCATGG TCATCCCCTG
 801 CCAGCGTCGA CTTCATGGAA GAAGTGACAC CTAAGAGCGT CAGTACCCCA
 851 TCAGTTGACT TGAGCCAGGA TGGAGATCAG GAGGGTATGG ATACCACACA
 901 GGTGGATGCA GAGAGCATAT ATGGAgACAG CACAGAGTAT CAgGATGATA
 951 AAGAGTTTGG AATAGGTGAC CTCGTGTGGG GAAAGATCAA GGGCTTCTCC
1001 TGGTGGCCTG CCATGGTGGT GTCCTGGAAA GCCACCTCCA AgCGACAGGC
```

FIG. 1B-1

AMENDED SHEET

6/38

1051 CATGCCCGGA ATGCGCTGGG TACAGTGGTT TGGTGATGGC AAGTTTTCTG
1101 AGATCTCTGC TGACAAACTG GTGGCTCTGG GGCTGTTCAG CCAGCACTTT
1151 AATCTGGCTA CCTTCAATAA GCTGGTTTCT TATAGGAAGG CCATGTACCA
1201 CACTCTGGAG AAAGCCAGGG TTCGAGCTGG CAAGACCTTC TCCAGCAGTC
1251 CTGGAGAGTC ACTGGAGGAC CAGCTGAAGC CCATGCTGGA GTGGGCCCAC
1301 GGTGGCTTCA AGCCTACTGG GATCGAGGGC CTCAAACCCA ACAAGAAGCA
1351 ACCAGTGGTT AATAAGTCGA AGGTGCGTCG TTCAGACAGT AGGAACTTAG
1401 AACCCAGGAG ACGCGAGAAC AAAAGTCGAA GACGCACAAC CAATGACTCT
1451 GCTGCTTCTG AGTCCCCCCC ACCCAAGCGC CTCAAGACAA ATAGCTATGC
1501 CGGGAAGGAC CGAGGGGAGG ATGAGGAGAG CCGAGAACGG ATGGCTTCTG
1551 AAGTCACCAA CAACAAGGGC AATCTGGAAG ACCGCTGTTT GTCCTGTGGA
1601 AAGAAGAACC CTGTGTCCTT CCACCCCCTC TTTGAGGGTG GGCTCTGTCA
1651 GAGTTGCCGG GATCGCTTCC TAGAGCTCTT CTACATGTAT GATGAGGACG
1701 GCTATCAGTC CTACTGCACC GTGTGCTGTG AGGGCCGTGA ACTGCTGCTG
1751 TGCAGTAACA CAAGCTGCTG CAGATGCTTC TGTGTGGAGT GTCTGGAGCT
1801 GCTGGTGGGC GCAGGCACAG CTGAGGATGC CAAGCTGCAG GAACCCTGGA
1851 GCTGCTATAT GTGCCTCCCT CAGCGCTGCC ATGGGGTCCT CCGACGCAGG
1901 AAAGATTGGA ACATGCGCCT GCAAGACTTC TTCACTACTG ATCCTGACCT
1951 GGAAGAATTT GAGCCACCCA AGTTGTACCC AGCAATTCCT GCAGCCAAAA
2001 GGAGGCCCAT TAGAGTCCTG TCTCTGTTTG ATGGAATTGC AACGGGGTAC
2051 TTGGTGCTCA AGGAGTTGGG TATTAAAGtG GAAAAGTACA TTGCCTCCGA
2101 AGTCTGTGCA GAGTCCATCG CTGTGGGAAC TGTTAAGCAT GAAGGCCAGA
2151 TCAAATATGT CAATGACGTC CGGAAAATCA CCAAGAAAAA TATTGAAGAG
2201 TGGGGCCCGT TCGACTTGGT GATTGGTGGA AGCCCATGCA ATGATCTCTC

FIG. 1B-2

2251 TAACGTCAAT CCTGCCCGCA AAGGTTTATA TGAGGGCACA GGAAGGCTCT
2301 TCTTCGAGTT TTACCACTTG CTGAATTATA CCCGCCCCAA GGAGGGCGAC
2351 AACCCGTCCAT TCTTCTGGAT GTTCGAGAAT GTTGTGGCCA TGAAAGTGAA
2401 TGACAAGAAA GACATCTCAA GATTCCTGGC ATGTAACCCA GTGATGATCG
2451 ATGCCATCAA GGTGTCTGCT GCTCACAGGG CCCGGTACTT CTGGGGTAAC
2501 CTACCCGGAA TGAACAGGCC CGTGATGGCT TCAAAGAATG ATAAGCTCGA
2551 GCTGCAGGAC TGCCTGGAGT TCAGTAGGAC AGCAAAGTTA AAGAAAGTGC
2601 AGACAATAAC CACCAAGTCG AACTCCATCA GACAGGGCAA AAACCAGCTT
2651 TTCCCTGTAG TCATGAATGG CAAGGACGAC GTTTTGTGGT GCACTGAGCT
2701 CGAAAGGATC TTCGGCTTCC CTGCTCACTA CACGGACGTG TCCAACATGG
2751 GCCGCGGCGC CCGTCAGAAG CTGCTGGGCA GGTCCTGGAG TGTACCGGTC
2801 ATCAGACACC TGTTTGCCCC CTTGAAGGAC TACTTTGCCT GTGAATAGTT
2851 CTACCCAGGA CTGGGGAGCT CTCGGTCAGA GCCAGTGCCC AGAGTCACCC
2901 CTCCCTGAAG GCACCTCACC TGTCCCCTTT TTAGCTCACC TGTGTGGGGC
2951 CTCACATCAC TGTACCTCAG CTTTCTCCTG CTCAGTGGGA GCAGAGCCTC
3001 CTGGCCCTTG CAGGGGAGCC CCGGTGCTCC CTCCGTGTGC ACAGCTCAGA
3051 CCTGGCTGCT TAGAGTAGCC CGGCATGGTG CTCATGTTCT CTTACCCTGA
3101 AACTTTAAAA CTTGAAGTAG CTAGTAAGAT GGCTTTCTTT TACCCTCCTG
3151 AGTTTATCAC TCAGAAGTGA TGGCTAAGAT ACCAAAAAAA CAAACAAAAA
3201 CAGAAACAAA AAACAAAAAA AAACCTCAAC AGCTCTcTTA GTACTCAGGT
3251 TCATGCTGCA AAATCACTTG AGATTTTGTT TTTAAGTAAC CCGTGcTCcA
3301 CATTTGCTGG AGGATGCTAT TGTGAATGTG GGCTCAGATG AGCAAGGTCA
3351 AGGGGCCAAA AAAAATTCCC CCTCTCCCCC CAGGAGTATT TGAAGATGAT
3401 GTTTATGGTT TAAGTCTTCC TGGCACCTTC CCCTTGCTTT GGTACAAGGG

FIG. 1B-3

3451 CTGAAGTCCT GTTGGTCTTG TAGCATTTCC CAGGATGATG ATGTCAGCAG
3501 GGATGACATC ACCACCTTTA GGGCTTTTCC CTGGCAGGGG CCCATGTGGC
3551 TAGTCCTCAC GAAGACTGGA GTAGAATGTT TGGAGCTCAG GAAGGGTGGG
3601 TGGAGTGGCC CTCTTCCAGG TGTGAGGGAT ACGAAGGAGG AAGCTTAGGG
3651 AAATCCATTC CCCACTCCCT CTTGCCAAAT GAGGGGCCCA GTCCCCAACA
3701 GCTCAGGTCC CCAGAACCCC CTAGTTCCTC ATGAGAAGCT AGGACCAGAA
3751 GCACATCGTT CCCCTTATCT GAGCAGTGTT TGGGGAACTA CAGTGAAAAC
3801 CTTCTGGAGA TGTTAAAAGC TTTTTACCCC ACGATAGATT GTGTTTTTAA
3851 GGGGTGCTTT TTTTAGGGGC ATCACTGGAG ATAAGAAAGC TGCATTTCAG
3901 AAATGCCATC GTAATGGTTT TTAAACACCT TTTACCTAAT TACAGGTGCT
3951 ATTTTATAGA AGCAGACAAC ACTTCTTTTT ATGACTCTCA GACTTCTATT
4001 TTCATGTTAC CATTTTTTTT GTAACTCGCA AGGTGTGGGC TTTTGTAACT
4051 TCACAGGTGT GGGGAGAGAC TGCCTTGTTT CAACAGTTTG TCTCCACTGG
4101 TTTCTAATTT TTAGGTGCAA AGATGACAGA TGCCCAGAGT TTACCTTTCT
4151 GGTTGATTAA AGTTGTATTT CTCTAAAAAA AAAAAAAAAA AAAAA

FIG. 1B-4

AMENDED SHEET

Human DNMT3A DNA Sequence


```
   1 GGCCGGCGTC GACCGACAGC GAGCGGAGGG AGGGAGCGAG CGAGCGAGCA
  51 GCAGCGGCCG GGAGGGAGGG AGGGCGCGCG GGCGGCGGCG GCGGCGAGAG
 101 CAGAGGACGA GCCGGGACGC GGCGCCGCGG CACCAGGGCG CGCAGCCGGG
 151 CCGGCCCGAC CCCACCGGCC ATACGGTGGA GCCATCGAAG CCCCCACCCA
 201 CAGGCTGACA GAGGCACCGT TCACCAGAGG GCTCAACACC GGGATCTATG
 251 TTTAAGTTTT AACTCTCGCC TCCAAAGACC ACGATAATTC CTTCCCCAAA
 301 GCCCAGCAGC CCCCCAGCCC CGCGCAGCCC CAGCCTGCCT CCCGGCGCCC
 351 AGATGCCCGC CATGCCCTCC AGCGGCCCCG GGGACACCAG CAGCTCTGCT
 401 GCGGAGCGGG AGGAGGACCG AAAGGACGGA GAGGAGCAGG AGGAGCCGCG
 451 TGGCAAGGAG GAGCGCCAAG AGCCCAGCAC CACGGCACGG AAGGTGGGGC
 501 GGCCTGGGAG GAAGCGCAAG CACCCCCCGG TGGAAAGCGG TGACACGCCA
 551 AAGGACCCTG CGGTGATCTC CAAGTCCCCA TCCATGGCCC AGGACTCAGG
 601 CGCCTCAGAG CTATTACCCA ATGGGGACTT GGAGAAGCGG AGTGAGCCCC
 651 AGCCAGAGGA GGGGAGCCCT GCTGGGGGGC AGAAGGGCGG GGCCCCAGCA
 701 GAGGGAGAGG GTGCAGCTGA GACCCTGCCT GAAGCCTCAA GAGCAGTGGA
 751 AAATGGCTGC TGCACCCCCA AGGAGGGCCG AGGAGCCCCT GCAGAAGCGG
 801 GCAAAGAACA GAAGGAGACC AACATCGAAT CCATGAAAAT GGAGGGCTCC
 851 CGGGGCCGGC TGCGGGGTGG CTTGGGCTGG GAGTCCAGCC TCCGTCAGCG
 901 GCCCATGCCG AGGCTCACCT TCCAGGCGGG GGACCCCTAC TACATCAGCA
 951 AGCGCAAGCG GGACGAGTGG CTGGCACGCT GGAAAAGGGA GGCTGAGAAG
1001 AAAGCCAAGG TCATTGCAGG AATGAATGCT GTGGAAGAAA ACCAGGGGCC
1051 CGGGGAGTCT CACAAGGTGG AGGAGGCCAG CCCTCCTGCT GTGCAGCAGC
1101 CCACTGACCC CGCATCCCCC ACTGTGGCTA CCACGCCTGA GCCCGTGGGG
1151 TCCGATGCTG GGGACAAGAA TGCCACCAAA GCAGGCGATG ACGAGCCAGA
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AMENDED SHEET

FIG. 1C-1

1201 GTACGAGGAC GGCCGGGGCT TTGGCATTGG GGAGCTGGTG TGGGGGAAAC
1251 TGCGGGGCTT CTCCTGGTGG CCAGGCCGCA TTGTGTCTTG GTGGATGACG
1301 GGCCGGAGCC GAGCAGCTGA AGGCACCCGC TGGGTCATGT GGTTCGGAGA
1351 CGGCAAATTC TCAGTGGTGT GTGTTGAGAA GCTGATGCCG CTGAGCTCGT
1401 TTTGCAGTGC GTTCCACCAG GCCACGTACA ACAAGCAGCC CATGTACCGC
1451 AAAGCCATCT ACGAGGTCCT GCAGGTGGCC AGCAGCCGCG CGGGGAAGCT
1501 GTTCCCGGTG TGCCACGACA GCGATGAGAG TGACACTGCC AAGGCCGTGG
1551 AGGTGCAGAA CAAGCCCATG ATTGAATGGG CCCTGGGGGG CTTCcAGCAT
1601 TATGGCCCTA AGGGCCTGGA GCCACCAGAA GAAGAGAAGA ATCCCTACAA
1651 AGAAGTGTAC ACGGACATGT GGGTGGAACC TGAGGCAGCT GCATACGCAC
1701 CACCTCCACC AGCCAAAAAG CCCCGGAAGA GCACAGCGGA GAAGCCCAAG
1751 GTCAAGGAGA TTATTGATGA GCGCACAAGA GAGCGGcTGG TGTACGAGGT
1801 GCGGCAGAAG TGCCGGAACA TTGAGGACAT CTGCATCTCC TGTGGGAGCC
1851 TCAATGTTAC CCTGGAACAC CCCCTCTTCG TTGGAGGAAT GTGCCAAAAC
1901 TGCAAGAACT GCTTTCTGGA GTGTGCGTAC CAGTACGACG ACGACGGCTA
1951 CCAGTCCTAC TGCACCATCT GCTGTGGGGG CCGTGAGGTG CTCATGTGCG
2001 GAAACAACAA CTGCTGCAGG TGCTTTTGCG TGGAGTGTGT GGACCTCTTG
2051 GTGGGGCCGG GGGCTGCCCA gGCAGCCATT AAGGAAgACC CCTGGAACTG
2101 CTACATGTGC GGGCACAAGG GTACCTACGG GCTGCTGCGG CGGCGAAAGG
2151 ACTGGCCCTC CCGGCTCCAg ATGTTCTTCG CTAATAACCA CgACCAGgAA
2201 TTTGACCCTC CAAAGGTTTA CCCACCTGTC CCAGCTgAgA AAAGGAAGCC
2251 CATCCGGGTG CTGTCTCTCT TTGATGGAAT CGCTACAGGG CTCCTGGTGC
2301 TGAAGGACTT GGGCATTCAG GTGGACCGCT ACATTGCCTC GGAGGTGTGT

FIG. 1C-2

2351 GAGGACTCCA TCACGGTGGC CATGGTGCGG CACCAGGGGA AGATCATGTA
2401 CGTCGGGGAC GTCCGCAGCG TCACACAGAA GCATATCCAG GAGTGGGGCC
2451 CATTCGATCT GGTGATTGGG GGCAGTCCCT GCAATGACCT CTCCATCGTC
2501 AACCCTGCTC GCAAGGGCCT CTACGAGGGC ACTGGCCGGC TCTTCTTTGA
2551 GTTCTACCGC CTCCTGCATG ATGCGCGGCC CAAGGAGGGA GATGATCGCC
2601 CCTTCTTCTG GCTCTTTGAG AATGTGGTGG CCATGGGCGT TAGTGACAAG
2651 AGGGACATCT CGCGATTTCT CGAGTCCAAC CCTGTGATGA TTGATGCCAA
2701 AGAAGTGTCA GCTGCACACA GGGCCCGCTA CTTCTGGGGT AACCTTCCCG
2751 GTATGAACAG GCCGTTGGCA TCCACTGTGA ATGATAAGCT GGAGCTGCAG
2801 GAGTGTCTGG AGCATGGCAG GATAGCCAAG TTCAGCAAAG TGAGGACCAT
2851 TACTACGAGG TCAAACTCCA TAAAGCAGGG CAAAGACCAG CATTTTCCTG
2901 TCTTCATGAA TGAGAAAGAG GACATCTTAT GGTGCACTGA AATGGAAAGG
2951 GTATTTGGTT TCCCAGTCCA CTATACTGAC GTCTCCAACA TGAGCCGCTT
3001 GGCGAGGCAG AGACTGCTGG GCCGGTCATG GAGCGTGCCA GTCATCCGCC
3051 ACCTCTTCGC TCCGCTGAAG GAGTATTTTG CGTGTGTGTA AGGGACATGG
3101 GGGCAAACTG AGGTAGCGAC ACAAAGTTAA ACAAACAAAC AAAAAACACA
3151 AAACATAATA AAACACCAAG AACATGAGGA TGGAGAGAAG TATCAGCACC
3201 CAGAAGAGAA AAAGGAATTT AAAACAAAAA CCACAGAGGC GGAAATACCG
3251 GAGGGCTTTG CCTTGCGAAA AGGGTTGGAC ATCATCTCCT GATTTTTCAA
3301 TGTTATTCTT CAGTCCTATT TAAAAACAAA ACCAAGCTCC CTTCCCTTCC
3351 TCCCCCTTCC CTTTTTTTTC GGTCAGACCT TTTATTTTCT ACTCTTTTCA
3401 GAGGGGTTTT CTGTTTGTTT GGGTTTTGTT TCTTGCTGTG ACTGAAACAA
3451 GAAGGTTATT GCAGCAAAAA TCAGTAACAA AAAATAGTAA CAATACCTTG
3501 CACAGGAAAG GTGGGAGGAG AGGAAAAAAG GGAAATTTTT AAAGAAATCT

FIG. 1C-3

AMENDED SHEET

3551 ATATATTGGC TTGTTTTTTT TTTTGTTTTT TGTTTTTTTT TTTTGGGTTT
3601 TTTTTTTTTA CTATATATCT TTTTTTTGTT GTCTCTAGCC TGATCAGATA
3651 GGAGCACAAG CAGGGGACGG AAAGAGAGAG ACACTCAGGC GGCAGCATTC
3701 CCTCCCAGCC ACTGAGCTGT CGTGCCAGCA CCATTCCTGG TCACGCAAAA
3751 CAGAACCCAG TTAGCAGCAG GGAGACGAGA ACACCACACA AGACATTTTT
3801 CTACAGTATT TCAGGTGCCT ACCACACAGG AAACCTTGAA GAAAATCAGT
3851 TTCTAGAAGC CGCTGTTACC TCTTGTTTAC AGTTTATATA TATATGATAG
3901 ATATGAGATA TATATATAAA AGGTACTGTT AACTACTGTA CAACCCGACT
3951 TCATAATGGT GCTTTCAAAC AGCGAGATGA GTAAAAACAT CAGCTTCCAC
4001 GTTGCCTTCT GCGCAAAGGG TTTCACCAAG GATGGAGAAA GGGAGACAGC
4051 TTGCAGATGG CGCGTTCTCA CGGTGGGCTC TTCCCCTTGG TTTGTAACGA
4101 AGTGAAGGAG GAGAACTTGG GAGCCAGGTT CTCCCTGCCA AAAAGGGGGC
4151 TAGATGAGGT GGTCGGGCCC GTGGACAGCT GAGAGTGGGA TTCATCCAGA
4201 CTCATGCAAT AACCCTTTGA TTGTTTTCTA AAAGGAGACT CCCTCGGCAA
4251 GATGGCAGAG GGTACGGAGT CTTCAGGCCC AGTTTCTCAC TTTAGCCAAT
4301 TCGAGGGCTC CTTGTGGTGG GATCAGAACT AATCCAGAGT GTGGGAAAGT
4351 GACAGTCAAA ACCCCACCTG GAGCAAATAA AAAAACATAC AAAACGTAAA
4401 AAAAAAAAAA AAAAAA

FIG. 1C-4

AMENDED SHEET

Human DNMT3B1 DNA Sequence:

1 GGCCGCGAAT TCGGCACGAG CCCTGCACGG CCGCCAGCCG GCCTCCCGCC
51 AGCCAGCCCC GACCCGCGGC TCCGCCGCCC AGCCGCGCCC CAGCCAGCCC
101 TGCGGCAGGA AAGCATGAAG GGAGACACCA GGCATCTCAA TGGAGAGGAG
151 GACGCCGGCG GGAGGGAAGA CTCGATCCTC GTCAACGGGG CCTGCAGCGA
201 CCAGTCCTCC GACTCGCCCC CAATCCTGGA GGCTATCCGC ACCCCGGAGA
251 TCAGAGGCCG AAGATCAAGC TCGCGACTCT CCAAGAGGGA GGTGTCCAGT
301 CTGCTAAGCT ACACACAGGA CTTGACAGGC GATGGCGACG GGGAAGATGG
351 GGATGGCTCT GACACCCCAG TCATGCCAAA GCTCTTCCGG GAAACCAGGA
401 CTCGTTCAGA AAGCCCAGCT GTCCGAACTC GAAATAACAA CAGTGTCTCC
451 AGCCGGGAGA GGCACAGGCC TTCCCCACGT TCCACCCGAG GCCGGCAGGG
501 CCGCAACCAT GTGGACGAGT CCCCCGTGGA GTTCCCGGCT ACCAGGTCCC
551 TGAGACGGCG GGCAACAGCA TCGGCAGGAA CGCCATGGCC GTCCCCTCCC
601 AGCTCTTACC TTACCATCGA CCTCACAGAC GACACAGAGG ACACACATGG
651 GACGCCCCAG AGCAGCAGTA CCCCCTACGC CCGCCTAGCC CAGGACAGCC
701 AGCAGGGGGG CATGGAGTCC CCGCAGGTGG AGGCAGACAG TGGAGATGGA
751 GACAGTTCAG AGTATCAGGA TGGGAAGGAG TTTGGAATAG GGGACCTCGT
801 GTGGGGAAAG ATCAAGGGCT TCTCCTGGTG GCCCGCCATG GTGGTGTCTT
851 GGAAGGCCAC CTCCAAGCGA CAGGCTATGT CTGGCATGCG GTGGGTCCAG
901 TGGTTTGGCG ATGGCAAGTT CTCCGAGGTC TCTGCAGACA AACTGGTGGC
951 ACTGGGGCTG TTCAGCCAGC ACTTTAATTT GGCCACCTTC AATAAGCTCG
1001 TCTCCTATCG AAAAGCCATG TACCATGCTC TGGAGAAAGC TAGGGTGCGA
1051 GCTGGCAAGA CCTTCCCCAG CAGCCCTGGA GACTCATTGG AGGACCAGCT
1101 GAAGCCCATG TTGGAGTGGG CCCACGGGGG CTTCAAGCCC ACTGGGATCG
1151 AGGGCCTCAA ACCCAACAAC ACGCAACCAG TGGTTAATAA GTCGAAGGTG

FIG. 1D-1

1201 CGTCCTGCAG GCAGTAGGAA ATTAGAATCA AGGAAATACG AGAACAAGAC
1251 TCGAAGACGC ACAGCTGACG ACTCAGCCAC CTCTGACTAC TGCCCCGCAC
1301 CCAAGCGCCT CAAGACAAAT TGCTATAACA ACGGCAAAGA CCGAGGGGAT
1351 GAAGATCAGA GCCGAGAACA AATGGCTTCA GATGTTGCCA ACAACAAGAG
1401 CAGCCTGGAA GATGGCTGTT TGTCTTGTGG CAGGAAAAAC CCCGTGTCCT
1451 TCCACCCTCT CTTTGAGGGG GGGCTCTGTC AGACATGCCG GGATCGCTTC
1501 CTTGAGCTGT TTTACATGTA TGATGACGAT GGCTATCAGT CTTACTGCAC
1551 TGTGTGCTGC GAGGGCCGAG AGCTGCTGCT TTGCAGCAAC ACGAGCTGCT
1601 GCCGGTGTTT CTGTGTGGAG TGCCTGGAGG TGCTGGTGGG CACAGGCACA
1651 GCGGCCGAGG CCAAGCTTCA GGAGCCCTGG AGCTGCTACA TGTGTCTCCC
1701 GCAGCGCTGT CATGGCGTCC TGCGGCGCCG GAAGGACTGG AACGTGCGCC
1751 TGCAGGCCTT CTTCACCAGT GACACGGGGC TTGAATACGA AGCCCCCAAG
1801 CTGTACCCTG CCATTCCCGC AGCCCGAAGG CGGCCCATTC GAGTCCTGTC
1851 ATTGTTTGAT GGCATCGCGA CAGGCTACCT AGTCCTCAAA GAGTTGGGCA
1901 TAAAGGTAGG AAAGTACGTC GCTTCTGAAG TGTGTGAGGA GTCCATTGCT
1951 GTTGGAACCG TGAAGCACGA GGGGAATATC AAATACGTGA ACGACGTGAG
2001 GAACATCACA AAGAAAAATA TTGAAGAATG GGGCCCATTT GACTTGGTGA
2051 TTGGCGGAAG CCCATGCAAC GATCTCTCAA ATGTGAATCC AGCCAGGAAA
2101 GGCCTGTATG AGGGTACAGG CCGGCTCTTC TTCGAATTTT ACCACCTGCT
2151 GAATTACTCA CGCCCCAAGG AGGGTGATGA CCGGCCGTTC TTCTGGATGT
2201 TTGAGAATGT TGTAGCCATG AAGGTTGGCG ACAAGAGGGA CATCTCACGC
2251 TTCCTGGAGT GTAATCCAGT GATGATTGAT GCCATCAAAG TTTCTGCTGC
2301 TCACAGGGCC CGATACTTCT GGGGCAACCT ACCCGGGATG AACAGGCCCG
2351 TGATAGCATC AAAGAATGAT AAACTCGAGC TGCAGGACTG CTTGGAATAC
2401 AATAGGATAG CCAAGTTAAA GAAAGTACAG ACAATAACCA CCAAGTCGAA

FIG. 1D-2

2451 CTCGATCAAA CAGGGGAAAA ACCAACTTTT CCCTGTTGTC ATGAATGGCA
2501 AAGAAGATGT TTTGTGGTGC ACTGAGCTCG AAAGGATCTT TGGCTTTCCT
2551 GTGCACTACA CAGACGTGTC CAACATGGC CGTGGTGCCC GCCAGAAGCT
2601 GCTGGGAAGG TCCTGGAGCG TGCCTGTCAT CCGACACCTC TTCGCCCCTC
2651 TGAAGGACTA CTTTGCATGT GAATAGTTCC AGCCAGGCCC CAAGCCCACT
2701 GGGGTGTGTG GCAGAGCCAG GACCCAGGAG GTGTGATTCC TGAAGGCATC
2751 CCCAGGCCCT GCTCTTCCTC AGCTGTGTGG GTCATACCGT GTACCTCAGT
2801 TCCCTCTTGC TCAGTGGGG CAGAGCCACC TGACTCTTGC AGGGGTAGCC
2851 TGAGGTGCCG CCTCCTTGTG CACAAATCAG ACCTGGCTGC TTGGAGCAGC
2901 CTAACACGGT GCTCATTTTT TCTTCTCCTA AAACTTTAAA ACTTGAAGTA
2951 GGTAGCAACG TGGCTTTTTT TTTTTCCCTT CCTGGGTCTA CCACTCAGAG
3001 AAACAATGGC TAAGATACCA AAACCACAGT GCCGACAGCT CTCCAATACT
3051 CAGGTTAATG CTGAAAAATC ATCCAAGACA GTTATTGCAA GAGTTTAATT
3101 TTTGAAAACT GGGTACTGCT ATGTGTTTAC AGACGTGTGC AGTTGTAGGC
3151 ATGTAGCTAC AGGACATTTT TAAGGGCCCA GGATCGTTTT TTCCCAGGGC
3201 AAGCAGAAGA GAAAATGTTG TATATGTCTT TTACCCGGCA CATTCCCCTT
3251 GCCTAAATAC AAGGGCTGGA GTCTGCACGG GACCTATTAG AGTATTTTCC
3301 ACAATGATGA TGATTTCAGC AGGGATGACG TCATCATCAC ATTCAGGGCT
3351 ATTTTTTCCC CCACAAACCC AAGGGCAGGG GCCACTCTTA GCTAAATCCC
3401 TCCCCGTGAC TGCAATAGAA CCCTCTGGGG AGCTCAGGAA GGGGTGTGCT
3451 GAGTTCTATA ATATAAGCTG CCATATATTT TGTAGACAAG TATGGCTCCT
3501 CCATATCTCC CTCTTCCCTA GGAGAGGAGT GTGAAGCAAG GAGCTTAGAT
3551 AAGACACCCC CTCAAACCCA TTCCCTCTCC AGGAGACCTA CCCTCCACAG
3601 GCACAGGTCC CCAGATGAGA AGTCTGCTAC CCTCATTTCT CATCTTTTTA
3651 CTAAACTCAG AGGCAGTGAC AGCAGTCAGG GACAGACATA CATTTCTCAT

FIG. 1D-3

3701 ACCTTCCCCA CATCTGAGAG ATGACAGGGA AAACTGCAAA GCTCGGTGCT
3751 CCCTTTGGAG ATTTTTTAAT CCTTTTTTAT TCCATAAGAA GTCGTTTTTA
3801 GGGAGAACGG GAATTCAGAC AAGCTGCATT TCAGAAATGC TGTCATAATG
3851 GTTTTTAACA CCTTTTACTC TTCTTACTGG TGCTATTTTG TAGAATAAGG
3901 AACAACGTTG ACAAGTTTTG TGGGGCTTTT TATACACTTT TTAAAATCTC
3951 AAACTTCTAT TTTTATGTTT AACGTTTTCA TTAAAATTTT TTTGTAACTG
4001 GAGCCACGAC GTAACAAATA TGGGGAAAAA ACTGTGCCTT GTTTCAACAG
4051 TTTTTGCTAA TTTTTAGGCT GAAAGATGAC GGATGCCTAG AGTTTACCTT
4101 ATGTTTAATT AAAATCAGTA TTTGTCTAAA AAAAAAAAAA AAAAA

FIG. 1D-4

AMENDED SHEET

Mouse Dnmt3a Protein

```
  1 MPSSGPGDTS SSSLEREDDR KEGEEQEENR GKEERQEPSA TARKVGRPGR
 51 KRKHPPVESS DTPKDPAVTT KSQPMAQDSG PSDLLPNGDL EKRSEPQPEE
101 GSPAAGQKGG APAEGEGTET PPEASRAVEN GCCVTKEGRG ASAGEGKEQK
151 QTNIESMKME GSRGRLRGGL GWESSLRQRP MPRLTFQAGD PYYISKRKRD
201 EWLARWKRDA EKKAKVIAVM NAVEENQASG ESQKVEEASP PAVQQPTDPA
251 SPTVATTPEP VGGDAGDKNA TKAPDDEPEY EDGRGFGIGE LVWGKLRGFS
301 WWPGRIVSWW MTGRSRAAEG TRWVMWFGDG KFSVVCVEKL MPLSSFCSAF
351 HQATYNKQPM YRKAIYEVLQ VASSRAGKLF PACHDSDESD SGKAVEVQNK
401 QMIEWALGGF QPSGPKGLEP PEEEKNPYKE VYTDMWVEPE AAAYAPPPPA
451 KKPRKSTTEK PKVKEIIDER TRERLVYEVR QKCRNIEDIC ISCGSLNVTL
501 EHPFFIGGMC QNCKNCFLEC AYQYDDDGYQ SYCTICCGGR EVLMCGNNNC
551 CRCFCVECVD LLVGPGAAQA AIKEDPWNCY MCGHKGTYGL LRRREDWPSR
601 LQMFFANNHD QEFDPPKVYP PVPAEKRKPI RVLSLFDGIA TGLLVLKDLG
651 IQVDRYIASE VCEDSITVGM VRHQGKIMYV GDVRSVTQKH IQEWGPFDLV
701 IGGSPCNDLS IVNPARKGLY EGTGRLFFEF YRLLHDARPK EGDDRPFFWL
751 FENVVAMGVS DKRDISRFLE SNPVMIDAKE VSAAHRARYF WGNLPGMNRP
801 LASTVNDKLE LQECLEHGRI AKFSKVRTIT TRSNSIKQGK DQHFPVFMNE
851 KEDILWCTEM ERVFGFPVHY TDVSNMSRLA RQRLLGRSWS VPVIRHLFAP
901 LKEYFACV*
```

FIG. 2A

AMENDED SHEET

Mouse Dnmt3b1 Protein

1 MKGDSRHLNE EEGASGYEEC IIVNGNFSDQ SSDTKDAPSP PVLEAICTEP

51 VCTPETRGRR SSSRLSKREV SSLLNYTQDM TGDGDRDDEV DDGNGSDILM

101 PKLTRETKDT RTRSESPAVR TRHSNGTSSL ERQRASPRIT RGRQGRHHVQ

151 EYPVEFPATR SRRRRASSSA STPWSSPASV DFMEEVTPKS VSTPSVDLSQ

201 DGDQEGMDTT QVDAESIYGD STEYQDDKEF GIGDLVWGKI KGFSWWPAMV

251 VSWKATSKRQ AMPGMRWVQW FGDGKFSEIS ADKLVALGLF SQHFNLATFN

301 KLVSYRKAMY HTLEKARVRA GKTFSSSPGE SLEDQLKPML EWAHGGFKPT

351 GIEGLKPNKK QPVVNKSKVR RSDSRNLEPR RRENKSRRRT TNDSAASESP

401 PPKRLKTNSY GGKDRGEDEE SRERMASEVT NNKGNLEDRC LSCGKKNPVS

451 FHPLFEGGLC QSCRDRFLEL FYMYDEDGYQ SYCTVCCEGR ELLLCSNTSC

501 CRCFCVECLE VLVGAGTAED AKLQEPWSCY MCLPQRCHGV LRRRKDWNMR

551 LQDFFTTDPD LEEFEPPKLY PAIPAAKRRP IRVLSLFDGI ATGYLVLKEL

601 GIKVEKYIAS EVCAESIAVG TVKHEGQIKY VNDVRKITKK NIEEWGPFDL

651 VIGGSPCNDL SNVNPARKGL YEGTGRLFFE FYHLLNYTRP KEGDNRPFFW

701 MFENVVAMKV NDKKDISRFL ACNPVMIDAI KVSAAHRARY FWGNLPGMNR

751 PVMASKNDKL ELQDCLEFSR TAKLKKVQTI TTKSNSIRQG KNQLFPVVMN

801 GKDDVLWCTE LERIFGFPAH YTDVSNMGRG ARQKLLGRSW SVPVIRHLFA

851 PLKDYFACE*

FIG. 2B

AMENDED SHEET

Human DNMT3A Protein

1 MPAMPSSGPG DTSSSAAERE EDRKDGEEQE EPRGKEERQE PSTTARKVGR

51 PGRKRKHPPV ESGDTPKDPA VISKSPSMAQ DSGASELLPN GDLEKRSEPQ

101 PEEGSPAGGQ KGGAPAEGEG AAETLPEASR AVENGCCTPK EGRGAPAEAG

151 KEQKETNIES MKMEGSRGRL RGGLGWESSL RQRPMPRLTF QAGDPYYISK

201 RKRDEWLARW KREAEKKAKV IAGMNAVEEN QGPGESHKVE EASPPAVQQP

251 TDPASPTVAT TPEPVGSDAG DKNATKAGDD EPEYEDGRGF GIGELVWGKL

301 RGFSWWPGRI VSWWMTGRSR AAEGTRWVMW FGDGKFSVVC VEKLMPLSSF

351 CSAFHQATYN KQPMYRKAIY EVLQVASSRA GKLFPVCHDS DESDTAKAVE

401 VQNKPMIEWA LGGFQHYGPK GLEPPEEEKN PYKEVYTDMW VEPEAAAYAP

451 PPPAKKPRKS TAEKPKVKEI IDERTRERLV YEVRQKCRNI EDICISCGSL

501 NVTLEHPLFV GGMCQNCKNC FLECAYQYDD DGYQSYCTIC CGGREVLMCG

551 NNNCCRCFCV ECVDLLVGPG AAQAAIKEDP WNCYMCGHKG TYGLLRRRKD

601 WPSRLQMFFA NNHDQEFDPP KVYPPVPAEK RKPIRVLSLF DGIATGLLVL

651 KDLGIQVDRY IASEVCEDSI TVGMVRHQGK IMYVGDVRSV TQKHIQEWGP

701 FDLVIGGSPC NDLSIVNPAR KGLYEGTGRL FFEFYRLLHD ARPKEGDDRP

751 FFWLFENVVA MGVSDKRDIS RFLESNPVMI DAKEVSAAHR ARYFWGNLPG

801 MNRPLASTVN DKLELQECLE HGRIAKFSKV RTITTRSNSI KQGKDQHFPV

851 FMNEKEDILW CTEMERVFGF PVHYTDVSNM SRLARQRLLG RSWSVPVIRH

901 LFAPLKEYFA CV*

FIG. 2C

AMENDED SHEET

Human DNMT3B1 Protein

1 MKGDTRHLNG EEDAGGREDS ILVNGACSDQ SSDSPPILEA IRTPEIRGRR
51 SSSRLSKREV SSLLSYTQDL TGDGDGEDGD GSDTPVMPKL FRETRTRSES
101 PAVRTRNNNS VSSRERHRPS PRSTRGRQGR NHVDESPVEF PATRSLRRRA
151 TASAGTPWPS PPSSYLTIDL TDDTEDTHGT PQSSSTPYAR LAQDSQQGGM
201 ESPQVEADSG DGDSSEYQDG KEFGIGDLVW GKIKGFSWWP AMVVSWKATS
251 KRQAMSGMRW VQWFGDGKFS EVSADKLVAL GLFSQHFNLA TFNKLVSYRK
301 AMYHALEKAR VRAGKTFPSS PGDSLEDQLK PMLEWAHGGF KPTGIEGLKP
351 NNTQPVVNKS KVRRAGSRKL ESRKYENKTR RRTADDSATS DYCPAPKRLK
401 TNCYNNGKDR GDEDQSREQM ASDVANNKSS LEDGCLSCGR KNPVSFHPLF
451 EGGLCQTCRD RFLELFYMYD DDGYQSYCTV CCEGRELLLC SNTSCCRCFC
501 VECLEVLVGT GTAAEAKLQE PWSCYMCLPQ RCHGVLRRRK DWNVRLQAFF
551 TSDTGLEYEA PKLYPAIPAA RRRPIRVLSL FDGIATGYLV LKELGIKVGK
601 YVASEVCEES IAVGTVKHEG NIKYVNDVRN ITKKNIEEWG PFDLVIGGSP
651 CNDLSNVNPA RKGLYEGTGR LFFEFYHLLN YSRPKEGDDR PFFWMFENVV
701 AMKVGDKRDI SRFLECNPVM IDAIKVSAAH RARYFWGNLP GMNRPVIASK
751 NDKLELQDCL EYNRIAKLKK VQTITTKSNS IKQGKNQLFP VVMNGKEDVL
801 WCTELERIFG FPVHYTDVSN MGRGARQKLL GRSWSVPVIR HLFAPLKDYF
851 ACE*

FIG. 2D

AMENDED SHEET

```
Dnmt3a    1 MPSSGPGDTSSSSLEREDDRKEGEEQEENRGKEERQEPSATARKVGRPGR 50

Dnmt3a   51 KRKHPPVESSDTPKDPAVTTKSQPMAQDSGPSD....LLPNGDLEKRSEP 96

Dnmt3b    1 ................MKGDSRHLNEEEGASGYEECIIVNGNFSDQSSD 33

Dnmt3a   97 QPEEGSP....AAGQKGGAPAEGEGTETPPEAS.RAVENGCCVTKE..GR 139

Dnmt3b   34 TKDAPSPPVLEAICTEPVCTPETRGRRSSSRLSKREVSSLLNYTQDMTGD 83

Dnmt3a  140 G.....ASAGEG......KEQKQTNIESMKMEGSRGRLRGGLGWESSLRQ 178

Dnmt3b   84 GDRDDEVDDGNGSDILMPKLTRETKDTRTRSESPAVRTRHSNGTSSLERQ 133

Dnmt3a  179 RPMPRLTFQAGDPYYISKRKRDEWLARWKRDAEKKAKVIAVMNAVEENQA 228

Dnmt3b  134 RASPRITRGRQGRHHV.....QEYPVEFPATRSRRRRASSSASTPWSSPA 178

Dnmt3a  229 SGESQKVEEASPPAVQQPTDPASPTVATTPEPVGGDAGDKNATKAPDDEP 278

Dnmt3b  179 SVDF..MEEVTPKSVSTP....SVDLSQDGDQEGMDTTQVDAESIYGDST 222

Dnmt3a  279 EYEDGRGFGIGELVWGKLRGFSWWPGRIVSWWMTGRSRAAEGTRWVMWFG 328

Dnmt3b  223 EYQDDKEFGIGDLVWGKIKGFSWWPAMVVSWKATSKRQAMPGMRWVQWFG 272

Dnmt3a  329 DGKFSVVCVEKLMPLSSFCSAFHQATYNKQPMYRKAIYEVLQVASSRAGK 378

Dnmt3b  273 DGKFSEISADKLVALGLFSQHFNLATFNKLVSYRKAMYHTLEKARVRAGK 322

Dnmt3a  379 LFPACHDSDESDSGKAVEVQNKQMIEWALGGFQPSGPKGLEPPEEEK..N 426

Dnmt3b  323 TF.......SSSPGESLEDQLKPMLEWAHGGFKPTGIEGLKPNKKQPVVN 365

Dnmt3a  427 PYKEVYTDMW.VEP.............EAAAYAPPPPAKKPRKSTTEKPK 462

Dnmt3b  366 KSKVRRSDSRNLEPRRRENKSRRRTTNDSAASESPPPKRLKTNSYGGKDR 415
```

FIG.3A-1

AMENDED SHEET

```
Dnmt3a  463 VKEIIDERTRERLVYEVRQKCRNIEDICISCGSLNVTLEHPFFIGGMCQN 512
Dnmt3b  416 GE...DEESRERMASEVTNNKGNLEDRCLSCGKKNPVSFHPLFEGGLCQS 462

Dnmt3a  513 CKNCFLECAYQYDDDGYQSYCTICCGGREVLMCGNNNCCRCFCVECVDLL 562
Dnmt3b  463 CRDRFLELFYMYDEDGYQSYCTVCCEGRELLLCSNTSCCRCFCVECLEVL 512

Dnmt3a  563 VGPGAAQAAIKEDPWNCYMCGHKGTYGLLRRREDWPSRLQMFFANNHD.Q 611
Dnmt3b  513 VGAGTAEDAKLQEPWSCYMCLPQRCHGVLRRRKDWNMRLQDFFTTDPDLE 562

Dnmt3a  612 EFDPPKVYPPVPAEKRKPIRVLSLFDGIATGLLVLKDLGIQVDRYIASEV 661
Dnmt3b  563 EFEPPKLYPAIPAAKRRPIRVLSLFDGIATGYLVLKELGIKVEKYIASEV 612

Dnmt3a  662 CEDSITVGMVRHQGKIMYVGDVRSVTQKHIQEWGPFDLVIGGSPCNDLSI 711
Dnmt3b  613 CAESIAVGTVKHEGQIKYVNDVRKITKKNIEEWGPFDLVIGGSPCNDLSN 662

Dnmt3a  712 VNPARKGLYEGTGRLFFEFYRLLHDARPKEGDDRPFFWLFENVVAMGVSD 761
Dnmt3b  663 VNPARKGLYEGTGRLFFEFYHLLNYTRPKEGDNRPFFWMFENVVAMKVND 712

Dnmt3a  762 KRDISRFLESNPVMIDAKEVSAAHRARYFWGNLPGMNRPLASTVNDKLEL 811
Dnmt3b  713 KKDISRFLACNPVMIDAIKVSAAHRARYFWGNLPGMNRPVMASKNDKLEL 762

Dnmt3a  812 QECLEHGRIAKFSKVRTITTRSNSIKQGKDQHFPVFMNEKEDILWCTEME 861
Dnmt3b  763 QDCLEFSRTAKLKKVQTITTKSNSIRQGKNQLFPVVMNGKDDVLWCTELE 812

Dnmt3a  862 RVFGFPVHYTDVSNMSRLARQRLLGRSWSVPVIRHLFAPLKEYFACV*   909
Dnmt3b  813 RIFGFPAHYTDVSNMGRGARQKLLGRSWSVPVIRHLFAPLKDYFACE*   860
```

FIG.3A-2

AMENDED SHEET

```
DNMT3A    1 MPAMPSSGPGDTSSSAAEREEDRKDGEEQEEPRGKEERQEPSTTARKVGR

DNMT3A   51 PGRKRKHPPVESGDTPKDPAVISKSPSMAQDSGASELLPNGDLEKRSEPQ
DNMT3B    1 ..............MKGDTRHLNGEEDAGGREDSILVNGACSDQSSDSP

DNMT3A  101 PEEGSPAGGQKGGAPAEGEGAAETLPEASRAVENGCCTPKEGRGAPAEAG
DNMT3B   36 PILEAIRTPEIRGGWASSRLSKREVSSLLSYTQDLTGDGDGEDGDGSDTP

DNMT3A  151 KEQKETNIESMKMEGSRGRLRGGLGWESSLRQRPMPRLTFQAGDPYYISK
DNMT3B   86 VMPKLFRETRTRSESPAVRTRNNNSVSSRERHRPSPRSTRGRQGRNHVDE

DNMT3A  201 RKRDEWLARWKREAEKKAKVIAGMNAVEENQGPGESHKVEEASPPAVQQP
DNMT3B  136 SPVEFPATRSLRRRATASAGTPWPSPPSSYLTIDLTDDTEDTH..GTPQS

DNMT3A  251 TDPASPTVATTPEPVGSDAGDKNATKAGDDEPEYEDGRGFGIGELVWGKL
DNMT3B  184 SSTPYARLAQDSQQGGMESPQVEADSGDGDSSEYQDGKEFGIGDLVWGKI

DNMT3A  301 RGFSWWPGRIVSWWMTGRSRAAEGTRWVMWFGDGKFSVVCVEKLMPLSSF
DNMT3B  234 KGFSWWPAMVVSWKATSKRQAMSGMRWVQWFGDGKFSEVSADKLVALGLF

DNMT3A  351 CSAFHQATYNKQPMYRKAIYEVLQVASSRAGKLFPVCHDSDESDTAKAVE
DNMT3B  284 SQHFNLATFNKLVSYRKAMYHALEKARVRAGKTFP.......SSPGDSLE

DNMT3A  401 VQNKPMIEWALGGFQHYGPKGLEP....PEEEKNPYKEVYTDMWVE...
DNMT3B  327 DQLKPMLEWAHGGFKPTGIEGLKPNNTQPVVNKSKVRRAGSRKLESRKYE

DNMT3A  443 .......PEAAAYAPPPPAKKPRKSTAEKPKVKEIIDERTRERLVYEVRQ
DNMT3B  377 NKTRRRTADDSATSDYCPAPKRLKTNCYNNGKDRGDEDQSREQMASDVAN
```

FIG.3B-1

AMENDED SHEET

```
DNMT3A  486  KCRNIEDICISCGSLNVTLEHPLFVGGMCQNCKNCFLECAYQYDDDGYQS
                .:|| |:|||  |    |||| ||:|| |:. |||  | ||||||||
DNMT3B  427  NKSSLEDGCLSCGRKNPVSFHPLFEGGLCQTCRDRFLELFYMYDDDGYQS

DNMT3A  536  YCTICCGGREVLMCGNNNCCRCFCVECVDLLVGPGAAQAAIKEDPWNCYM
             |||:|| ||||.|:| |.|||||||||.:.||| | |  |  ::||.|||
DNMT3B  477  YCTVCCEGRELLLCSNTSCCRCFCVECLEVLVGTGTAAEAKLQEPWSCYM

DNMT3A  586  CGHKGTYGLLRRRKDWPSRLQMFFANNHDQEFDPPKVYPPVPAEKRKPIR
             |  .  :|.|||||||  ||| ||..    |:: ||.|| :|| :|:|||
DNMT3B  527  CLPQRCHGVLRRRKDWNVRLQAFFTSDTGLEYEAPKLYPAIPAARRRPIR

DNMT3A  636  VLSLFDGIATGLLVLKDLGIQVDRYIASEVCEDSITVGMVRHQGKIMYVG
             ||||||||||| ||||:|||.| :|:||||||:|| || |:|:| | ||
DNMT3B  577  VLSLFDGIATGYLVLKELGIKVGKYVASEVCEESIAVGTVKHEGNIKYVN

DNMT3A  686  DVRSVTQKHIQEWGPFDLVIGGSPCNDLSIVNPARKGLYEGTGRLFFEFY
             |||.:|.|.|:|||||||||||||||||| ||||||||||||||||||||
DNMT3B  627  DVRNITKKNIEEWGPFDLVIGGSPCNDLSNVNPARKGLYEGTGRLFFEFY

DNMT3A  736  RLLHDARPKEGDDRPFFWLFENVVAMGVSDKRDISRFLESNPVMIDAKEV
              ||. .||||||||||||:||||||| | |||||||||| ||||||| .|
DNMT3B  677  HLLNYSRPKEGDDRPFFWMFENVVAMKVGDKRDISRFLECNPVMIDAIKV

DNMT3A  786  SAAHRARYFWGNLPGMNRPLASTVNDKLELQECLEHGRIAKFSKVRTITT
             |||||||||||||||||||. .. |||||||:|||: ||||  ||.||||
DNMT3B  727  SAAHRARYFWGNLPGMNRPVIASKNDKLELQDCLEYNRIAKLKKVQTITT

DNMT3A  836  RSNSIKQGKDQHFPVFMNEKEDILWCTEMERVFGFPVHYTDVSNMSRLAR
             :||||||||.| ||| || |||:|||||:||:||||||||||||| | ||
DNMT3B  777  KSNSIKQGKNQLFPVVMNGKEDVLWCTELERIFGFPVHYTDVSNMGRGAR

DNMT3A  886  QRLLGRSWSVPVIRHLFAPLKEYFACV*
             |:|||||||||||||||||||:||||
DNMT3B  827  QKLLGRSWSVPVIRHLFAPLKDYFACE*
```

FIG.3B-2

AMENDED SHEET

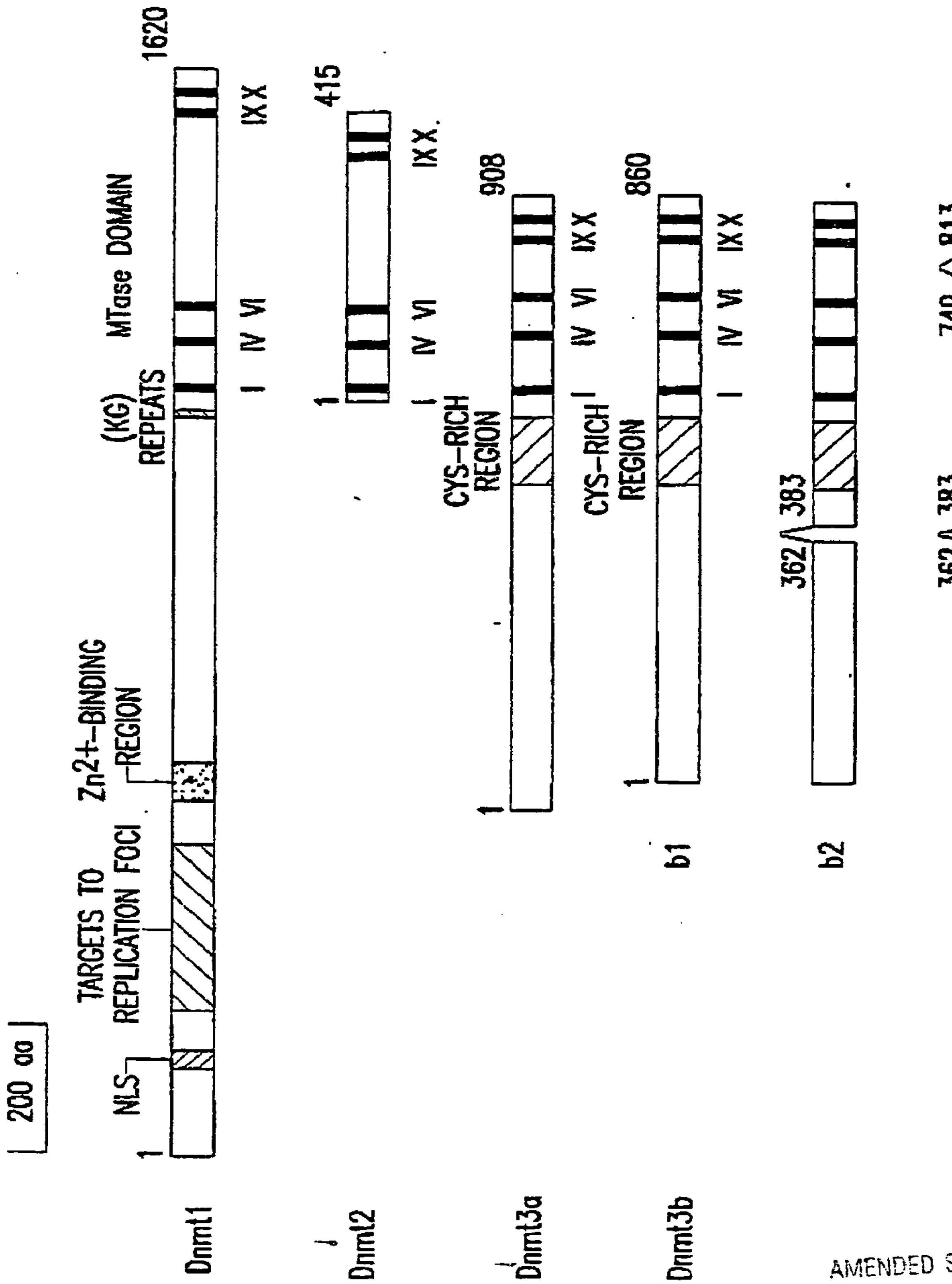
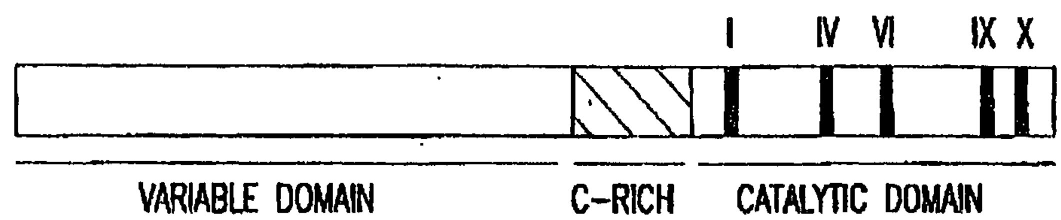


FIG. 4A

AMENDED SHEET



DNMT3A	100%	100%	100%
DNMT3B	28%	57%	81%
Zmt3	23%	52%	70%

FIG. 4B

AMENDED SHEET

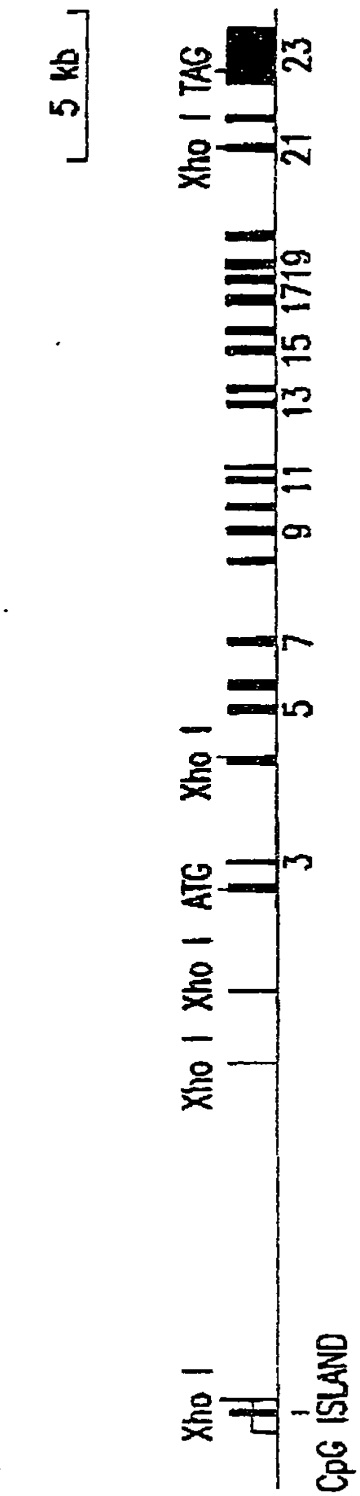


FIG. 4C

AMENDED SHEET

09/720086


```
Exon1  (>=90bp)CGGCAGgtgagcgccccgggg.intron(17618bp).tggcttctcccacagGAAAGC
Exon2  ( 148bp)TCAGAGgtggctgggcagtgg.intron(  887bp).CTGTTTCCTCTACAGGCCGAA
Exon3  (  62bp)ACACAGgtatggtctctgctc.intron( 3343bp).tgtttccttataaagGACTTG
Exon4  ( 102bp)CCAGCTgtaagtagccacacc.intron( 1642bp).ctctcttgcttctagGTCCGA
Exon5  ( 125bp)ACCAGGgttgttccccagatg.intron(  602bp).tccttctgtccacagTCCCTG
Exon6  ( 222bp)TATCAGgtatggccgagaggg.intron( 1403bp).tgggttttcttccagGATGGG
Exon7  ( 159bp)TCCGAGgtgagtccggggaag.intron( 2588bp).gtctttctcttttagGTCTCT
Exon8  ( 108bp)CTGGAGgtaacatgggatgag.intron(  917bp).actctgcctttgcagAAAGCT
Exon9  ( 145bp)AACCAGgtgggaatgagtccc.intron(  765bp).ttttcccctcaaaagTGGTTA
Exon10 (  60bp)AATACGgtatttccttcctgt.intron( 1813bp).aattacctttcacagAGAACA
Exon11 ( 126bp)GCCGAGgtgattgttgggtac.intron(  115bp).ttcttttctcaatagAACAAA
Exon12 (  45bp)TGGAAGgtaacgttctctccc.intron( 1095bp).ctgtttttcttacagATGGCT
Exon13 (  80bp)TGCCGGgtaagtcctcctact.intron(  417bp).ctctctggctgccagGATCGC
Exon14 ( 113bp)CTGCCGgtgagcactgggccc.intron( 1160bp).tgccactgggtccagGTGTTT
Exon15 ( 184bp)GAATACgtaagccacaggctc.intron(  600bp).ttccttacctggcagGAAGCC
Exon16 (  85bp)CGACAGgtgagttcggggaac.intron(  824bp).ctctggcccccacagGCTACC
Exon17 ( 146bp)AAAAATgtgagggcagtctgt.intron(  536bp).gtctctctctttcagATTGAA
Exon18 (  91bp)TGTATGgtgagcatccttctc.intron(  352bp).cttttctgagcacagAGGGTA
Exon19 ( 149bp)CTGGAGgtgagggaatctggg.intron(  958bp).tctttctccccacagTGTAAT
Exon20 (  86bp)GAACAGgtaacaaagggctct.intron( 2867bp).tttggctgttcccagGCCCGT
Exon21 (  70bp)GCCAAGttaaagaaagtacag.intron(  801bp).catttgttctccagTTAAAG
Exon22 ( 119bp)CGAAAGgtgagcaaggctgca.intron( 1434bp).ctccggtacccccagGATCTT
Exon23 (1585bp)
```

FIG.4D

AMENDED SHEET

	I	IV	VI
DNMT1	DVFSGCGGLSEGFHQAG	DVEMLCGGPPCQGFSGMNR	YRPRFFLLENVRNFVSFKR
Dnmt1	DVFSGCGGLSEGFHQAG	DVEMLCGGPPCQGFSGMNR	YRPRFFLLENVRNFVSYRR
MET1(Ath)	DIFAGCGGLSHGLKKAG	QVDFINGGPPCQGFSGMNR	FRPRYFLLENVRTFVSFNK
Masc1	DTFCGGGGVSLGARQAG	HVDILHLSPPCQTFSRAHT	VRPRLFTVEETDGIMDRQS
Masc2	DIFAGCGGLTLGLDLSG	EVDFIYGGPPCQGFSGVNR	YKPRFVLLENVKGLITTKL
Dnmt2	ELYSGIGGMHHALRESH	SFNMILMSPPCQPFTRIGL	KLPKYILLENVKGFEVSST
M.Spr	SLFSGIGAFEAALRNIG	EFDLLVGGSPCQSFSVAGH	KQPKFFVFENVKGLINHDK
DNMT3A	SLFDGIATGLLVLKDLG	PFDLVIGGSPCNDLSIVNP	DRPFFWLFENVVAMGVSDK
Dnmt3a	SLFDGIATGLLVLKDLG	PFDLVIGGSPCNDLSIVNP	DRPFFWLFENVVAMGVSDK
DNMT3B	SLFDGIATGYLVLKELG	PFDLVIGGSPCNDLSNVNP	DRPFFWMFENVVAMKVGDK
Dnmt3b	SLFDGIATGYLVLKELG	PFDLVIGGSPCNDLSNVNP	NRPFFWMFENVVAMKVNDK
Zmt3	SLFDGIATGYLVLRDLG	PFDLLIGGSPCNDLSIVNP	PQPFFWLFENVTFMQTHVK
consensus	--F-G-----------G	------GG-PC---S--N-	--P-F---ENV--------

	IX	X
DNMT1	RVVSVRECARSQGFP	LFGNILDKHRQVGNAVPPPLAKAIG
Dnmt1	RVVSVRECARSQGFP	FFGNILDRHRQVGNAVPPPLAKAIG
MET1(Ath)	RILTVRECARSQGFP	FAGNINHKHRQIGNAVPPPLAFALG
Masc1	RKFTVRELACIQGFP	FVGTLTDKRRIIGNAVPPPLSAAIM
Masc2	RVYTVRELARAQGFP	GLGGVKKWHRNIGNAVPVPLGEQIG
Dnmt2	RYFTPKEIANLQGFP	EKTTVKQRYRLLGNSLNVHVVAKLL
M.Spr	RRLTPLECFRLQAFD	AGISNSQLYKQTGNSITVTVLESIF
DNMT3A	DILWCTEMERVFGFP	SNMSRLARQRLLGRSWSVPVIRHLF
Dnmt3a	DILWCTEMERVFGFP	SNMSRLARQRLLGRSWSVPVIRHLF
DNMT3B	DVLWCTELERIFGFP	SNMGRGARQKLLGRSWSVPVIRHLF
Dnmt3b	DVLWCTELERIFGFP	SNMGRGARQKLLGRSWSVPVIRHLF
Zmt3	DHIWITELEKIFGFP	KSMGRPORQRVLGKSWSVPVIRHLL
consensus	------E--R--GFP	---------R--G-----P------

FIG. 5A

```
DNMT3A       EDICISCG......SLNVTLEHPLFVGGMCQNCKNCFLECAYQYDDDGYQSYCT
Dnmt3a       EDICISCG......SLNVTLEHPFFIGGMCQNCKNCFLECAYQYDDDGYQSYCT
DNMT3B       EDGCLSCG......RKNPVSFHPLFEGGLCQTCRDRFLELFYMYDDDGYQSYCT
Dnmt3b       EDRCLSCG......KKNPVSFHPLFEGGLCQSCRDRFLELFYMYDEDGYQSYCT
Zmt3         EDFCLSCG......SMSVDIIHPLFEGKLCTNCKFNFTETLYRYDEDGYQSYCT
ATRX_Human   IVSCTACGQQVNHFQKDSIYRHPSLQVLICKNCFKYYMSDDISRDSDGMDEQCR
ATRX_Mouse   IVSCTACGQQVNHFQKDSIYRHPSLQVLICKNCFKYYMSDDISRDSDGMDEQCR
Consensus       C  C                         C  C                C

DNMT3A       ICCGGREVLMCGNNNCCRCFCVECVDLLVGPGAAQAAIKE.DPWNCYMCGHKGT
Dnmt3a       ICCGGREVLMCGNNNCCRCFCVECVDLLVGPGAAQAAIKE.DPWNCYMCGHKGT
DNMT3B       VCCEGRELLLCSNTSCCRCFCVECLEVLVGTGTAAEAKLQ.EPWSCYMCLPQRC
Dnmt3b       VCCEGRELLLCSNTSCCRCFCVECLEVLVGAGTAEDAKLQ.EPWSCYMCLPQRC
Zmt3         VCCSGMEVILCAHDSCCRSFCVDCLDILVCQGTFDRLKNV.DPWTCYLCAPETS
ATRX_Human   WCAEGGNLICC..DFCHNAFCKKCILRNLGRKELSTIMDENNQWYCYICHPEPL
ATRX_Mouse   WCAEGGNLICC..DFCHNAFCKKCILRNLGRKELSTIMDENNQWYCYICHPEPL
Consensus     C         C    C    C  C                       C  C
```

FIG.5B

AMENDED SHEET

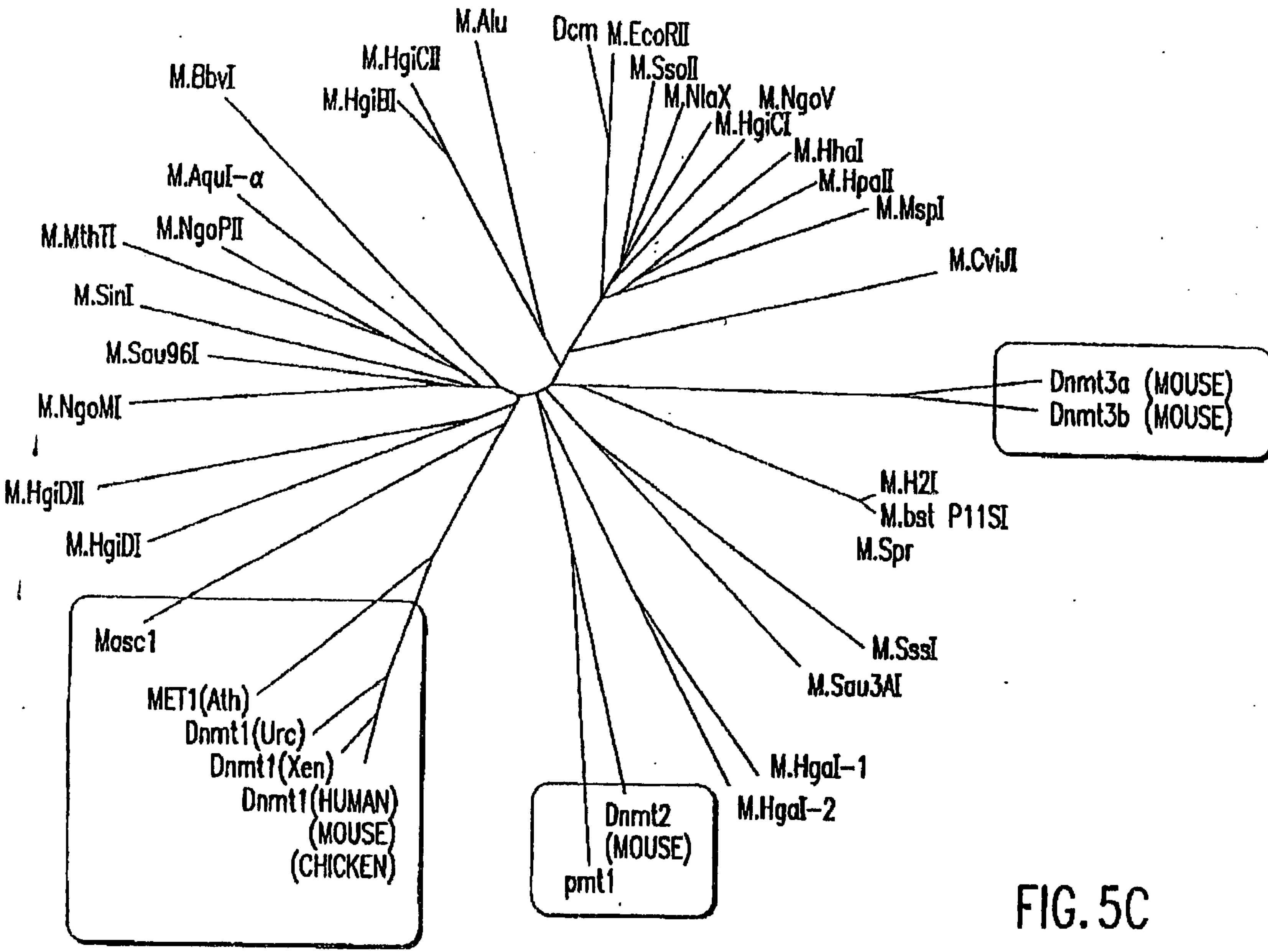


FIG. 5C

AMENDED SHEET

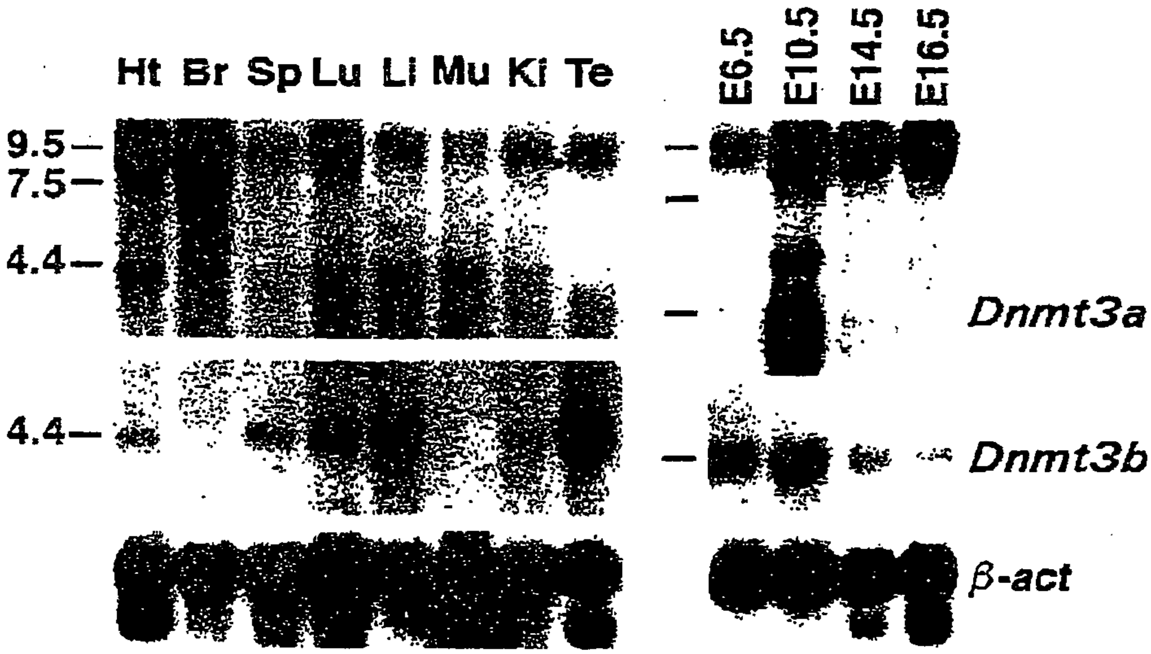
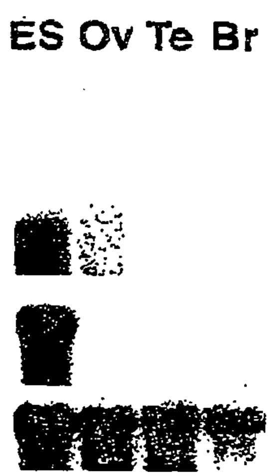


FIG.6A



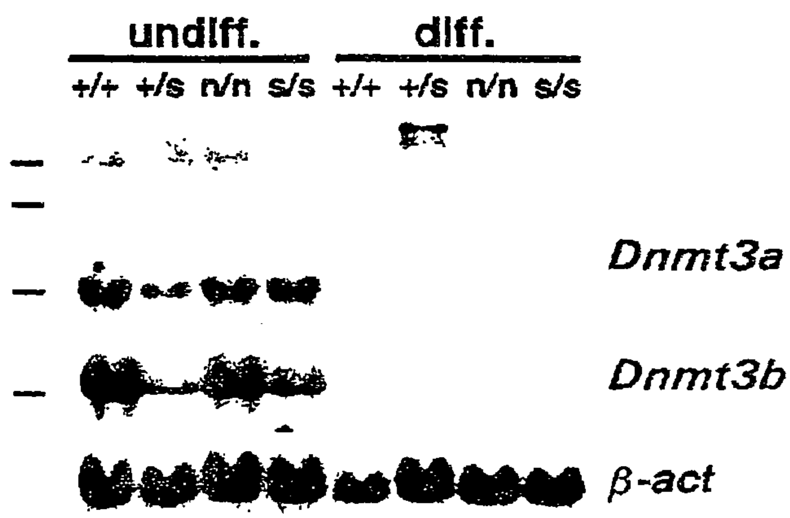


FIG.6B FIG.6C

AMENDED SHEET

Dnmt1

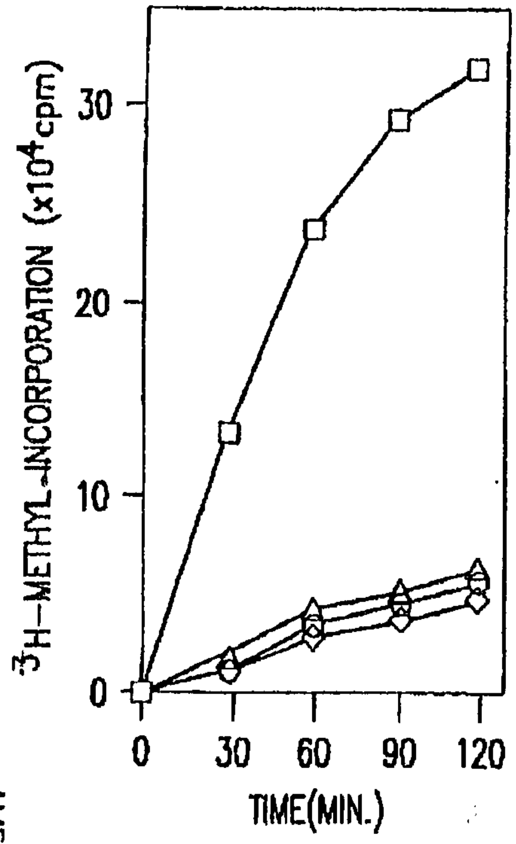


FIG. 7A

Dnmt3a

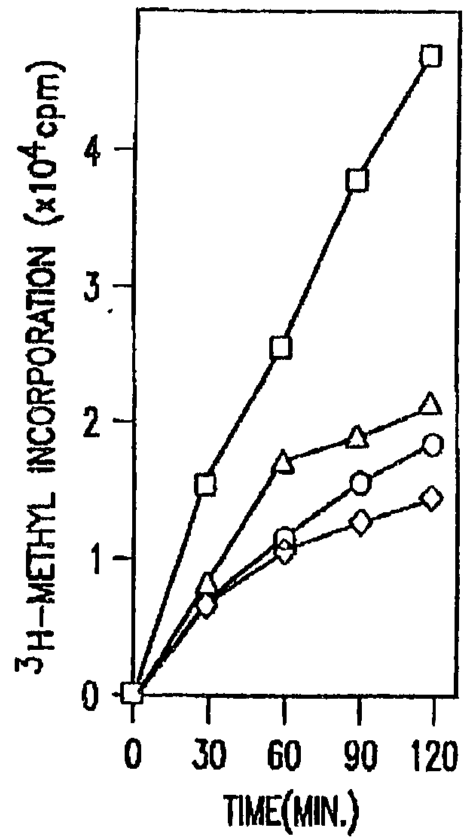


FIG. 7B

Dnmt3b

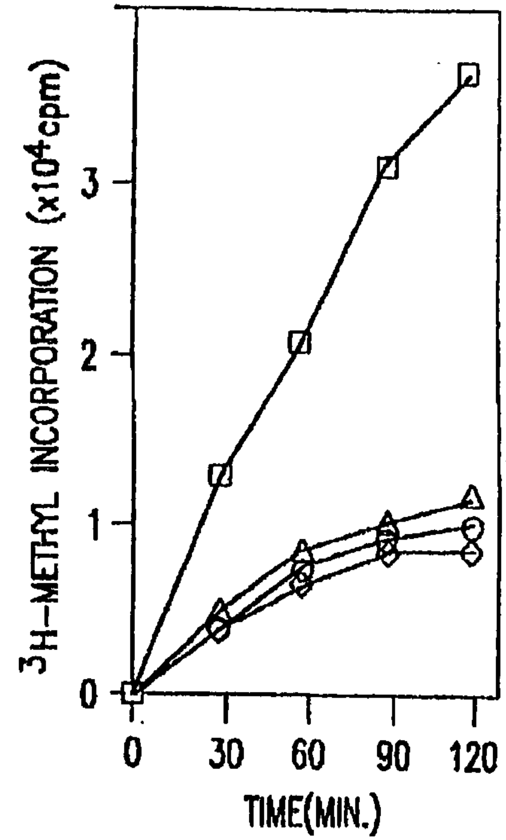


FIG. 7C

AMENDED SHEET

FIG.7D

AMENDED SHEET

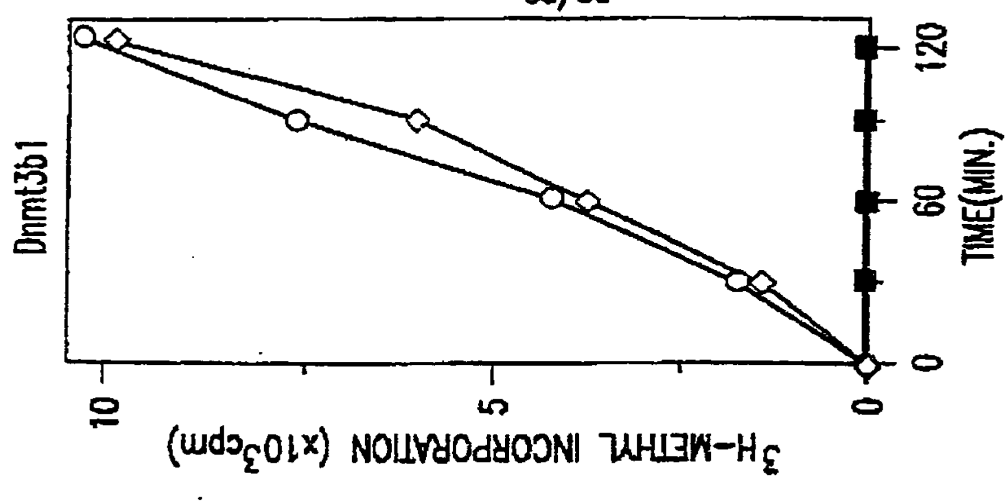


FIG. 8C

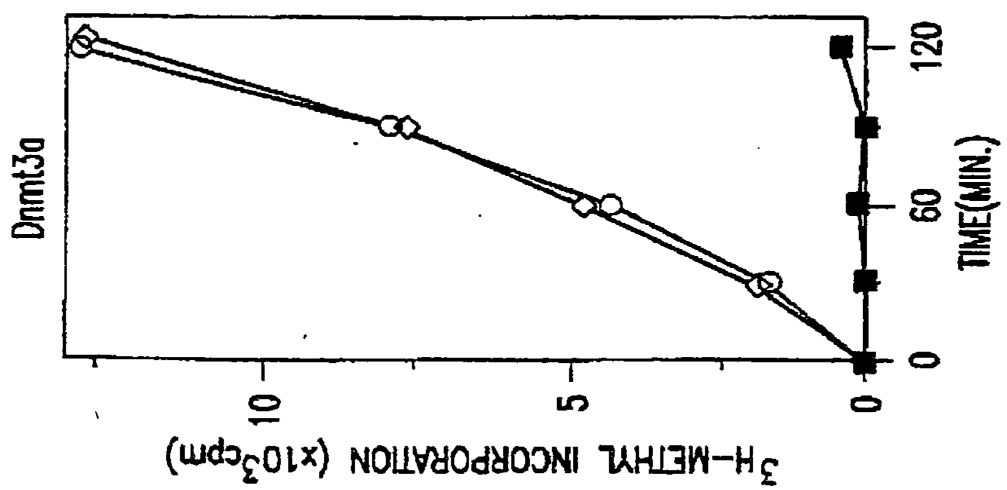


FIG. 8B

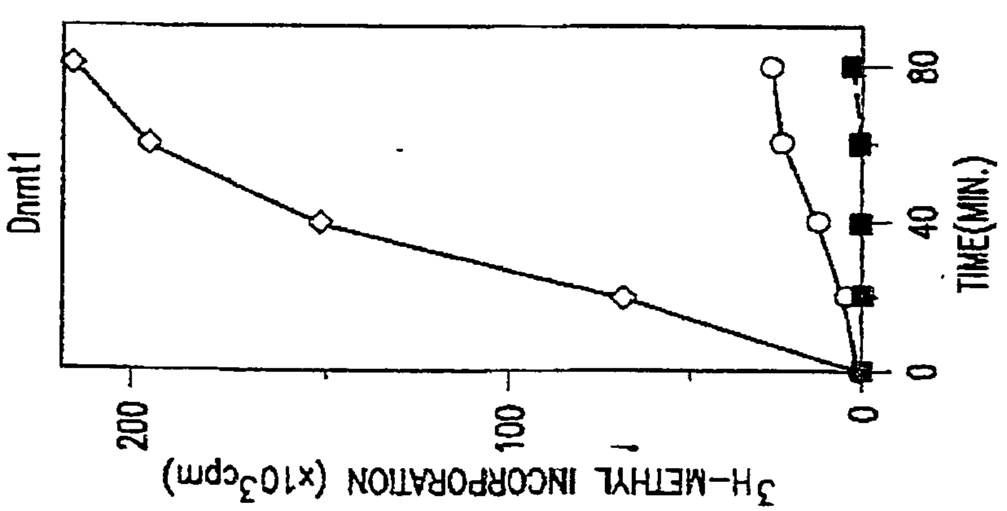


FIG. 8A

AMENDED SHEET

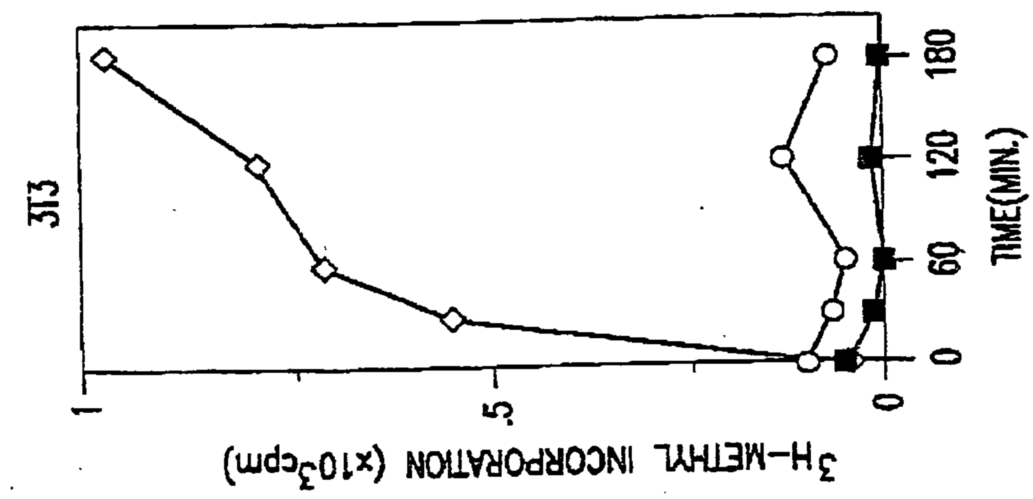

3T3
^{3}H-METHYL INCORPORATION (x10^{3}cpm)
1
.5
0
0
60
120
180
TIME(MIN.)

FIG. 8E

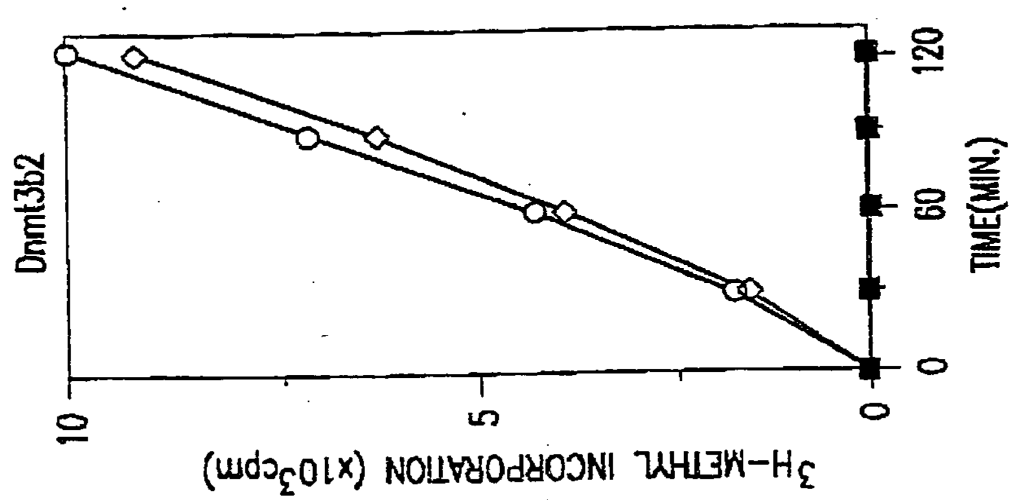

Dnmt3b2
^{3}H-METHYL INCORPORATION (x10^{3}cpm)
10
5
0
0
60
120
TIME(MIN.)

FIG. 8D

37/38

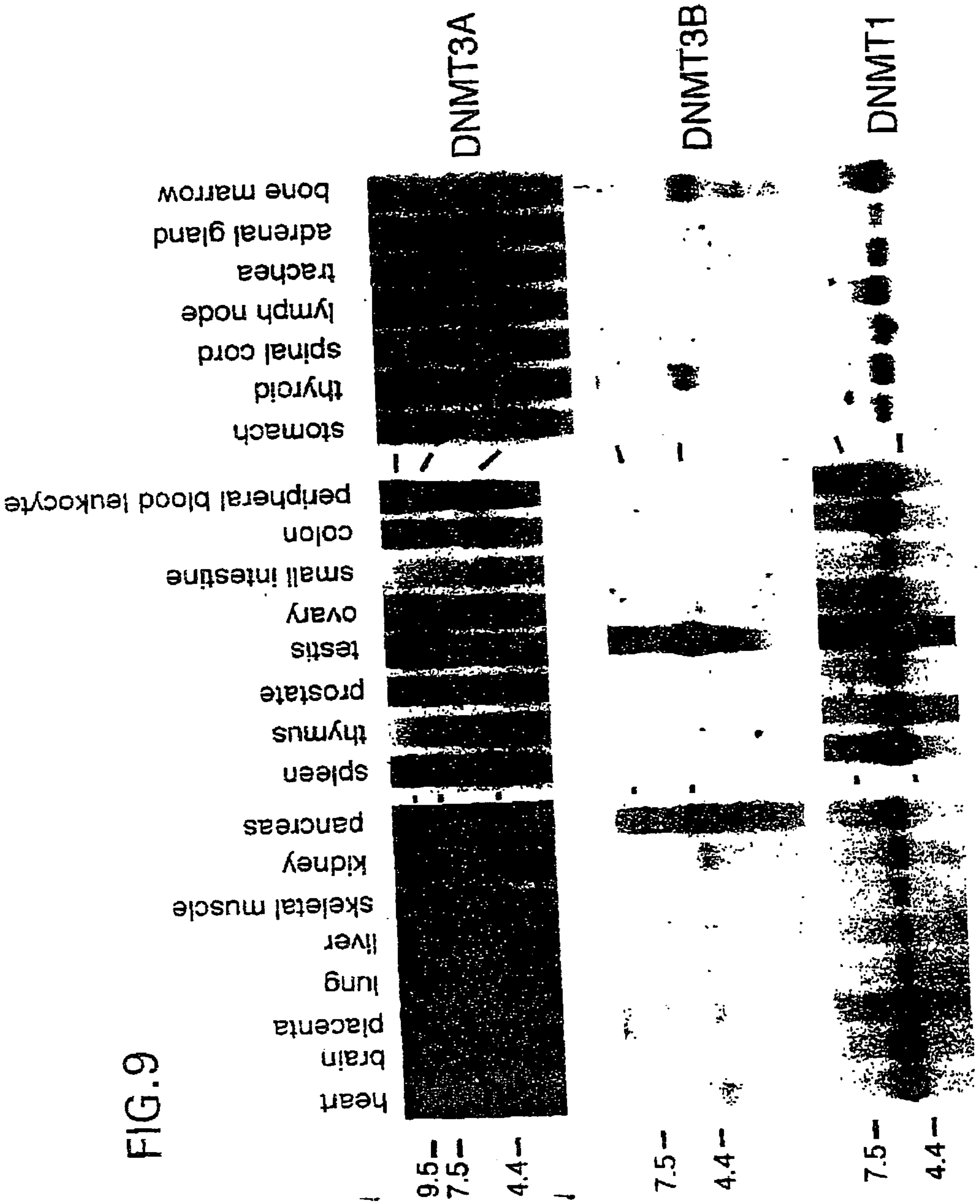


FIG.9

AMENDED SHEET

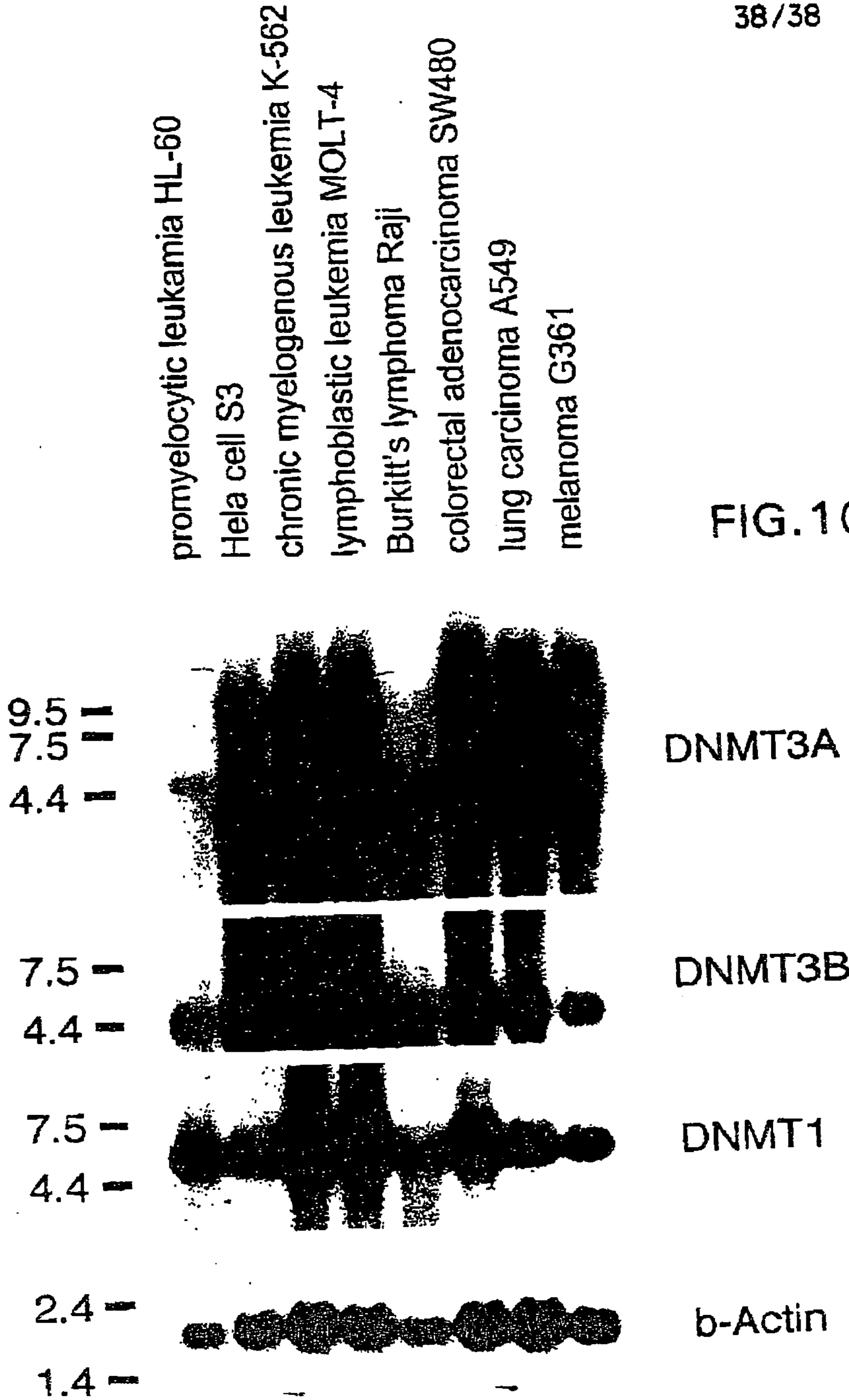


FIG.10

AMENDED SHEET